

O'Bryen, Barbara

From: Seharaseyon, Jegatheesan
Sent: Wednesday, September 29, 2004 11:28 AM
To: O'Bryen, Barbara
Subject: 09/526437

Hi,

Can you please do an interference search SEQ ID NO:2 and a word search of the protein, with a word size of 6 amino acid for 09/526,437

Thanks a lot!

Seyon.

J.Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

100



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 178391

TO: Jegatheesan Seharaseyon
Art Unit: 1647
Location: REM-4C61/4C70
Serial Number: 09/526437

Thursday, February 09, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

10/10/10

STIC-Biotech/ChemLib

178391

From: Seharaseyon, Jegatheesan
Sent: 78224 Wednesday, February 01, 2006 5:30 PM
To: STIC-Biotech/ChemLib
Subject: 09/526437

CRFE

Please search SEQ ID NO: 2 in the interference and pending databases.
Please also search a word size of 30.

Thanks.
J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

2-701 ad
LB

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

vendors:

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OM protein - protein search, using sw model

Run on: September 29, 2004, 12:34:27 ; Search time 125 Seconds
(without alignments)
906.412 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 401
Sequence: 1 MNKLKCALVFLDISIKWT.....QKLFLEMIGNVQSVKISCL 401

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2729

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401	100.0	401	2	AAV05742 Tumour ne
2	401	100.0	401	2	AAW95030 Tumour ne
3	401	100.0	401	2	AAW83926 Human FTH
4	401	100.0	401	2	AAW18715 A human t
5	401	100.0	401	4	AAW60570 Human TNF
6	401	100.0	401	6	AAW65245 Human TRA
7	401	100.0	401	6	AAO31135 Human TRA
8	401	100.0	401	2	AAO01625 Human ost
9	398	99.3	401	2	AAW99925 Full leng
10	398	99.3	401	2	AAW53239 Human OCI
11	398	99.3	401	2	AAW8622 Osteoclas
12	398	99.3	401	6	AAW70997 Human ost
13	398	99.3	401	7	AAW37427 Human ost
14	396	98.8	399	2	AAW99942 Mutated O
15	391	97.5	391	2	AAW53238 Human OCI
16	391	97.5	395	2	AAW57636 Modified
17	391	97.5	395	2	AAW18716 Carboxy t
18	388	96.8	393	2	AAW99948 Mutated O
19	380	94.8	380	2	AAW99924 Mature os
20	380	94.8	380	6	AAO19638 Human mil
21	358	89.3	390	2	AAW99937 Human tum
22	348	86.3	351	2	AAW99943 Mutated O
23	338	84.3	360	2	AAW99936 Mutated O
24	319	79.6	401	2	AAW99935 Mutated O
25	315	78.6	321	2	AAW99949 Mutated O

26	315	78.6	401	2	AAW99934 Mutated O
27	300	74.8	401	2	AAW38345 Human ost
28	300	74.8	401	3	AAW43400 Osteoprot
29	300	74.8	401	4	AAW66976 Human OPG
30	300	74.8	401	5	ABG71823 Wild type
31	300	74.8	401	6	ABP55109 Human ost
32	300	74.8	401	6	AAE34363 Human ost
33	300	74.8	401	7	ADD01627 Human ost
34	299	74.6	400	6	ABU08820 Human ost
35	297	74.1	401	2	AAW99931 Mutated O
36	297	74.1	401	2	AAW99932 Mutated O
37	279	69.6	380	4	AAW66988 Murine OP
38	279	69.6	537	6	AAO19639 Human mil
39	276	68.8	359	2	AAW99937 Mutated O
40	270	67.3	327	2	AAW99941 Mutated O
41	269	67.1	322	2	AAW99944 Mutated O
42	267	66.6	349	2	AAW83928 Human FTH
43	255	63.6	360	2	AAW99938 Mutated O
44	229	57.1	401	5	ABG73894 Human OPG
45	220	54.9	373	6	ABG73071 Human ost

ALIGNMENTS

RESULT 1
AAV05742 standard; protein; 401 AA.
AAV05742;
19-JUL-1999 (first entry)
Tumour necrosis factor receptor TR1.
Tumour necrosis factor receptor TR1.
Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist;
antagonist; screening; human; cancer; AIDS; Alzheimer's disease;
inflammation; arthritis; septicemia; autoimmune disease; psoriasis;
inflammatory bowel disease; transplant rejection;
graft versus host disease; infection; stroke; ischaemia;
acute respiratory disease syndrome; restenosis; brain injury;
bone disease; atherosclerosis; therapy.
Homo sapiens.
EP911633-A1.
28-APR-1999.
02-OCT-1998; 98EP-00203332.
08-OCT-1997; 97US-0061334P.
(SMIK) SMITHKLINE BEECHAM CORP.
McDonnell PC, Young PR, Zou J;
WPI; 1999-246560/21.
Identifying agonists and antagonists of tumor necrosis factor related
receptors TR1, TR3 and TR5, and of ligand TR3, useful for treatment of
cancer, AIDS, Alzheimer's disease, bone disease etc.
Disclosure; Page 10-12; 23pp; English.
The present sequence represents tumor necrosis factor receptor (TNFR)
TR1, also known as osteoprotegerin. The invention relates to TNFR related
polypeptides TR1, TR3 and TR5 (see AAV05742-44) and their ligand TR3 (see
AAV05745). TR1, TR3, TR5 and TR3 are used in claimed methods of
identifying agonists and antagonists, i.e. compounds that bind to the
receptors or ligand, and which activate (agonist) or inhibit activation
of (antagonists) TR1, TR3, TR5 or TR3. A screening kit for identifying
agonists, antagonists, ligands, receptors, substrates, enzymes etc. for

CC TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and
 CC antagonists are useful for treatment of chronic and acute inflammation,
 CC arthritis, septicemia, autoimmune disease e.g. inflammatory bowel
 CC disease, psoriasis, transplant rejection, graft versus host disease,
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,
 CC resection, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's disease,
 CC etc., caused by imbalance of TR1, TR3, TR5 or TL3
 XX
 SQ Sequence 401 AA:

Query Match 100.0%; Score 401; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETPPKYLHYDETSQHLCDKCPRTYKONCTAKMT 60
 DB 1 MNKLCCALVFLDISIKMTTQETPPKYLHYDETSQHLCDKCPRTYKONCTAKMT 60
 QY 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNHRVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNHRVCEKGRYLEIEFCLK 120
 QY 121 HRSCEPFGVVOAGTPERNTVCKRCPDGFSNETSSKAPCRKATNCSVFGILLTQKGNAT 180
 DB 121 HRSCEPFGVVOAGTPERNTVCKRCPDGFSNETSSKAPCRKATNCSVFGILLTQKGNAT 180
 QY 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRVAVPTKFTPMNLVLYVNDLPGTKVAESVERI 240
 DB 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRVAVPTKFTPMNLVLYVNDLPGTKVAESVERI 240
 QY 241 KROHSSQEQTFQLLKMKHQNKDQDIVKKIIDDIDCENSVO RHIGHANLTFFQLSLME 300
 DB 241 KROHSSQEQTFQLLKMKHQNKDQDIVKKIIDDIDCENSVO RHIGHANLTFFQLSLME 300
 QY 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRKNGDDOTLKGLMALKHSKTYHFPKT 360
 DB 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRKNGDDOTLKGLMALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 2
 AAM95030
 ID AAM95030 standard; protein; 401 AA.
 XX
 AC AAM95030;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE Tumour necrosis factor receptor (TNF-R) related polypeptide TR1.
 XX
 XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
 KM inflammation; septicemia; autoimmune disease; transplant rejection;
 KM graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 KM acute respiratory disease syndrome; resection, bone disease; cancer;
 KM atherosclerosis; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN EP897114-A2.
 XX
 PD 17-FEB-1999.
 XX
 PF 04-JUN-1998; 98EP-00304424.
 XX
 PR 13-AUG-1997; 97US-0055513P.
 PR 26-AUG-1997; 97US-0056980P.
 PR 29-AUG-1997; 97US-0057550P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
 PI Brigham-Burke MR, Young PR;
 XX
 DR WPI; 1999-134308/12.
 XX
 PT Identifying agonists and antagonists to tumour necrosis factor receptor
 PT (TNF-R) related polypeptides (TR1, TR2, TR3 and TR4) - useful for
 PT treating stroke, Alzheimer's disease and AIDS.
 XX
 PS Disclosure; Page 11-12; 18pp; English.

CC The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TR2,
 CC and TR4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TR2 or TR4; or (ii) contacting TR2
 CC or TR4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TR2 or TR4. TR and TR agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TR or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC resection, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
 CC Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR1
 XX
 SQ Sequence 401 AA:

Query Match 100.0%; Score 401; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETPPKYLHYDETSQHLCDKCPRTYKONCTAKMT 60
 DB 1 MNKLCCALVFLDISIKMTTQETPPKYLHYDETSQHLCDKCPRTYKONCTAKMT 60
 QY 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNHRVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNHRVCEKGRYLEIEFCLK 120
 QY 121 HRSCEPFGVVOAGTPERNTVCKRCPDGFSNETSSKAPCRKATNCSVFGILLTQKGNAT 180
 DB 121 HRSCEPFGVVOAGTPERNTVCKRCPDGFSNETSSKAPCRKATNCSVFGILLTQKGNAT 180
 QY 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRVAVPTKFTPMNLVLYVNDLPGTKVAESVERI 240
 DB 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRVAVPTKFTPMNLVLYVNDLPGTKVAESVERI 240
 QY 241 KROHSSQEQTFQLLKMKHQNKDQDIVKKIIDDIDCENSVO RHIGHANLTFFQLSLME 300
 DB 241 KROHSSQEQTFQLLKMKHQNKDQDIVKKIIDDIDCENSVO RHIGHANLTFFQLSLME 300
 QY 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRKNGDDOTLKGLMALKHSKTYHFPKT 360
 DB 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRKNGDDOTLKGLMALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 3
 AAM83926
 ID AAM83926 standard; protein; 401 AA.
 XX
 AC AAM83926;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Human FTHMA-070 protein.
 XX
 KM FTHMA-070; human; neurological disorder; therapy; diagnosis.
 XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 XX Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..401
 FT /label= Mac_protein
 XX
 XX WO9848051-A2.
 XX
 XX 29-OCT-1998.
 PD
 XX 17-APR-1998; 98WO-US007714.
 PF
 XX 18-APR-1997; 97US-0044746P.
 PR 10-OCT-1997; 97US-0062017P.
 XX
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 XX McCarthy SA, Holtzman D;
 PI
 XX WPI: 1999-024021/02.
 DR
 DR N-PSDB; AAV69277.
 XX
 XX New isolated human FTHMA-070 and T85 proteins - used to develop products
 PT for the diagnosis and therapy of disorders involving cellular processes,
 PT e.g. neuronal development.
 XX
 XX Claim 8; Fig 1; 127pp; English.
 PS
 XX This is the amino acid sequence of human FTHMA-070, a novel protein
 CC having homology to tumour necrosis factor receptor. The sequence was
 CC deduced from that of a cDNA clone (see AAV69277) isolated from a cardiac
 CC coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and
 CC polypeptides of the invention are useful as modulating agents in
 CC regulating a variety of cellular processes. They can be used for
 CC identifying compounds which bind to or modulate the activity of the
 CC polypeptides (claimed). They can also be used in screening assays,
 CC detection assays (e.g. chromosomal mapping, tissue typing, forensic
 CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,
 CC monitoring clinical trials, and pharmacogenomics), and methods of
 CC treatment (e.g. therapeutic and prophylactic) e.g. for neurological
 CC disorders
 CC
 XX Sequence 401 AA;
 SQ
 Query Match 100.0%; Score 401; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 VTQSUKTIRFLHSFTMYKLYOKLPLEMIGNOVOSVKISCL 401
 DB 361 VTQSUKTIRFLHSFTMYKLYOKLPLEMIGNOVOSVKISCL 401
 RESULT 4
 ID AAB18715 standard; protein; 401 AA.
 XX AAB18715;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 XX A human tumour necrosis factor family receptor (TR1).
 XX
 XX Human; tumour necrosis factor family receptor; TR1; tumour growth;
 KW cell proliferation; chlamydia infection; immunodeficiency; septic shock;
 KW T-cell mediated autoimmune disease; acquired immunodeficiency syndrome;
 KW AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia;
 KW apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis;
 KW inflammatory disease; atherosclerosis; diabetes mellitus; allergy;
 KW neurological disorder; autoimmune disease; wound healing; bone formation;
 KW osteoporosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FH Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..401
 FT /note= "mature protein"
 XX
 XX WO200054651-A2.
 XX
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US006592.
 PF
 XX 15-MAR-1999; 99US-0124489P.
 PR 26-MAY-1999; 99US-0136248P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Greene JM, Fleischmann RD, Ni J;
 PI
 XX WPI: 2000-618858/59.
 DR N-PSDB; AAA75736.
 XX
 XX Novel tumor necrosis factor family receptor for diagnosing and treating
 PT acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
 PT inflammatory diseases and autoimmune diseases.
 XX
 PS Claim 13; Fig 1A-B; 228pp; English.
 XX
 XX The present sequence represents a human tumour necrosis factor family
 CC receptor (TR1) polypeptide. An agonist to the TR1 receptor is useful for
 CC inhibiting tumour growth, to stimulate human cellular proliferation, to
 CC regulate immune response and antiviral response, to protect against the
 CC effects of ionising radiations, to protect against chlamydia infections,
 CC to regulate growth, and to treat immunodeficiencies such as in human
 CC immunodeficiency virus (HIV). An antagonist to the TR1 receptor is useful
 CC for treating T-cell mediated autoimmune diseases, acquired
 CC immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft
 CC rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TR1
 CC polypeptides and polypeptides, and TR1 agonists and antagonists are
 CC useful for treating cancers, cardiovascular diseases, inflammatory
 CC diseases, atherosclerosis, diabetes mellitus, neurological disorders,
 CC autoimmune diseases, for promoting angiogenesis, for treating allergy,
 CC for wound healing, for regulating bone formation and for treating
 CC osteoporosis
 XX
 XX Sequence 401 AA;
 SQ

Query Match 100.0%; Score 401; DB 3; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKMKT 60
 QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQCNRTNHRVCECKEGRYLIEFCLK 120
 DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQCNRTNHRVCECKEGRYLIEFCLK 120
 QY 121 HRSCEPFGVQVQATPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSCEPFGVQVQATPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNICGSNBSSTQKCGIDVTLCEBAFFRAVPKFTPNMLSVLDNLPGTKVAESVERI 240
 DB 181 HDNICGSNBSSTQKCGIDVTLCEBAFFRAVPKFTPNMLSVLDNLPGTKVAESVERI 240
 QY 241 KRQSSQEQTFQLLKLMKQKQNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLME 300
 DB 241 KRQSSQEQTFQLLKLMKQKQNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLME 300
 QY 301 SLPGKTVGABDIKTIKACKPSDQILKLSLRIRKNGDQTLKGLMHALKHSTYHPKPT 360
 DB 301 SLPGKTVGABDIKTIKACKPSDQILKLSLRIRKNGDQTLKGLMHALKHSTYHPKPT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 5

AAB60570 standard; protein; 401 AA.

AC AAB60570;

DT 18-APR-2001 (first entry)

DE Human TNFRSF11B protein.

XX Human; TNFRSF11B; osteoclastogenesis inhibitory factor;

KM single nucleotide polymorphism; SNP; osteoclast recruitment;

KM osteoclast function; osteoporosis; metastatic bone disease;

KM Paget's disease; rheumatoid arthritis; periodontal bone disease.

XX Homo sapiens.

OS WO200104137-A1.

PN 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US018803.

PR 09-JUL-1999; 99US-0143020P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC,

DR WPI: 2001-147175/15.

XX N-PSDB; AAF69948.

PT Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising single

XX nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's

XX disease and rheumatoid arthritis.

PS Claim 10; Fig 4; 11app; English.

XX The present sequence is the human osteoclastogenesis inhibitory factor

CC (TNFRSF11B). Polynucleotides comprising one or more of twenty four novel
 CC single nucleotide polymorphisms in the TNFRSF11B gene have been
 CC identified. TNFRSF11B regulate osteoclast recruitment and function. An
 CC understanding of variations in the gene should thus be useful in
 CC developing new therapies for metabolic disorders caused by abnormal
 CC osteoclast recruitment and function such as osteoporosis, metastatic bone
 CC disease, Paget's disease, rheumatoid arthritis and periodontal bone
 CC disease

XX Sequence 401 AA;

QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKMKT 60
 QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQCNRTNHRVCECKEGRYLIEFCLK 120
 DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQCNRTNHRVCECKEGRYLIEFCLK 120
 QY 121 HRSCEPFGVQVQATPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSCEPFGVQVQATPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNICGSNBSSTQKCGIDVTLCEBAFFRAVPKFTPNMLSVLDNLPGTKVAESVERI 240
 DB 181 HDNICGSNBSSTQKCGIDVTLCEBAFFRAVPKFTPNMLSVLDNLPGTKVAESVERI 240
 QY 241 KRQSSQEQTFQLLKLMKQKQNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLME 300
 DB 241 KRQSSQEQTFQLLKLMKQKQNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLME 300
 QY 301 SLPGKTVGABDIKTIKACKPSDQILKLSLRIRKNGDQTLKGLMHALKHSTYHPKPT 360
 DB 301 SLPGKTVGABDIKTIKACKPSDQILKLSLRIRKNGDQTLKGLMHALKHSTYHPKPT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 6

AAB36245 standard; protein; 401 AA.

AC AAB36245;

DT 26-JUN-2003 (first entry)

DE Human TRAIL receptor protein, TR1.

XX TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;

KM hyperproliferative disorder; neurodegenerative disorder; immune disorder;

KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;

KM retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;

KM rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;

KM glomerulonephritis; immune deficiency syndrome; myasthenia gravis;

KM infectious disease; acquired immunodeficiency syndrome; viral infection;

KM AIDS; proliferative disorder; myelodysplastic syndrome; aplastic anemia;

KM ischemic injury; myocardial infarction; reperfusion injury; cachexia;

KM anorexia; stroke; cardiovascular disorder; peripheral artery disease;

XX limb ischaemia; arhythmia; congestive heart failure; neovascularisation;

XX ocular disorder; wound healing; angiogenesis; transplantation; human.

OS Homo sapiens.

XX WO200297033-A2.

PD 05-DEC-2002.
 XX 07-MAY-2002; 2002MO-US014256.
 XX 25-MAY-2001; 2001US-0293473P.
 PR 04-JUN-2001; 2001US-0294981P.
 PR 02-AUG-2001; 2001US-0309176P.
 PR 21-SEP-2001; 2001US-0323807P.
 PR 09-OCT-2001; 2001US-0327364P.
 PR 07-NOV-2001; 2001US-0331044P.
 PR 14-NOV-2001; 2001US-0331310P.
 PR 20-DEC-2001; 2001US-0341237P.
 PR 05-APR-2002; 2002US-0369860P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ,
 PI WPI, 2003-140454/13.
 DR WPI, 2003-140454/13.
 XX Novel antibody useful for treating cancers and other hyperproliferative
 PT disorders, immunospecifically binds to TRAIL receptor and comprises
 PT variable heavy or light chain complementarity determining regions.
 XX Example 2; Page 275-276; 301pp; English.
 PS The present invention relates to novel antibodies that immunospecifically
 XX bind to TRAIL receptor (TR4). Sequences of the invention are useful for
 CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.
 CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in
 CC human. They are useful for detecting expression of TR4 polypeptide and
 CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-
 CC proliferative disorders. Antibodies of the invention are useful for
 CC treating, preventing or ameliorating neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),
 CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,
 CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,
 CC polyomyelitis, immune-related glomerulonephritis, myasthenia gravis,
 CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory
 CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS),
 CC herpes viral infections and other viral infections) and proliferative
 CC disorders. They are also useful for treating myelodysplastic syndromes
 CC (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke,
 CC myocardial infarction and reperfusion injury), septic shock, cachexia,
 CC anorexia and toxin-induced liver diseases (such as alcohol). They are
 CC also useful for treating cardiovascular disorders including peripheral
 CC artery diseases such as limb ischaemia, arrhythmia, congestive heart
 CC failure and cardiovascular tuberculozoid, diseases or disorders associated
 CC with neovascularisation and ocular disorders, for wound healing, for
 CC promoting angiogenesis and as adjuvants to enhance immune responsiveness
 CC to specific antigen e.g. viral antigen. They are also useful in the
 CC preparation or recovery from surgery, trauma, radiation therapy and
 CC transplantation. The present sequence is human TR1 protein used in the
 CC invention
 CC XX
 SQ Sequence 401 AA;
 Query Match 100.0%; Score 401; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 HRSCEPGGVVQAGTPERNYVCKRCPCDPGFSNETSXKAPCRKHTNCSVFGLLTQKGNAT 180
 QY 181 HDNICSGNSESTQKCGIDVLTCEBAFFRFAVPTFTPTNWLVLVDNLTPTVNAESVERI 240
 DB 181 HDNICSGNSESTQKCGIDVLTCEBAFFRFAVPTFTPTNWLVLVDNLTPTVNAESVERI 240
 QY 241 KROHSSOEOTFQILKIMWQKQDDIVKIIQDDIDLCENSQVRHGHANLTFEOLRLIME 300
 DB 241 KROHSSOEOTFQILKIMWQKQDDIVKIIQDDIDLCENSQVRHGHANLTFEOLRLIME 300
 QY 301 SLPGKVGAEDIEKTIKACRPSDQILKLSMRKNGQDQTLKGLMALKSKTYHPKPT 360
 DB 301 SLPGKVGAEDIEKTIKACRPSDQILKLSMRKNGQDQTLKGLMALKSKTYHPKPT 360
 QY 361 VTOSLKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401
 DB 361 VTOSLKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401
 RESULT 7
 ID AA031135 standard; protein; 401 AA.
 AC AA031135;
 XX 06-OCT-2003 (first entry)
 DT Human TRAIL receptor 1.
 XX Human TRAIL receptor 1.
 DE Human; protein coordinate data; heavy chain variable domain; VH; cancer;
 KW complementarity determining region; CDR, light chain variable domain; VL;
 KW TRAIL receptor 7; TR7; tumour necrosis factor; KILR; death receptor 5;
 KW DR3; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
 KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
 KW glioblastoma; graft versus host disease; antibody therapy; neoplastic;
 KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
 KW immunosuppressive; neuroprotective; antibody therapy; osteoprotegerin;
 KW OPG; osteoclastogenesis inhibitory factor; OCIF; TNFRSF11B; FTHMA-090.
 KW OS Homo sapiens.
 XX MO2003054216-A2.
 XX 03-JUL-2003.
 PD 19-DEC-2002; 2002WO-US040597.
 PF 20-DEC-2001; 2001US-0341237P.
 PR 05-APR-2002; 2002US-0369877P.
 PR 04-JUN-2002; 2002US-0384828P.
 PR 18-JUL-2002; 2002US-0396591P.
 PR 15-AUG-2002; 2002US-0403370P.
 PR 13-NOV-2002; 2002US-0425737P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ,
 PI WPI, 2003-569250/53.
 DR WPI, 2003-569250/53.
 PT New antibody or its fragment, useful for treating, preventing or
 PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
 PT disease, AIDS.
 XX Disclosure; Page 269-270; 301pp; English.
 XX The invention relates to an isolated antibody or its fragments such as
 CC VHCDR1 (heavy chain variable domain complementarity determining region),
 CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
 CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
 CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related

CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
 CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and Killer. The
 CC antibody or its fragment is useful for treating, preventing or
 CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
 CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
 CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
 CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
 CC a neurodegenerative disorder. The invention is useful in antibody
 CC therapy. The present sequence is human TR1. TR1 is also referred to as
 CC osteoprotegerin (OPG), osteoclastogenesis inhibitory factor (OCIF),
 CC TNFRSF11B and FTHMA-090
 CC
 XX
 SQ Sequence 401 AA:
 Query Match 100.0%; Score 401; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEBTSQQLCDKCPGTYLKQHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEBTSQQLCDKCPGTYLKQHTAKMKT 60
 QY 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNRTNHRVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNRTNHRVCEKGRYLEIEFCLK 120
 QY 121 HRSCPPGFGVQAQTPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSCPPGFGVQAQTPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNIGSGNSESTQKCGIDVTLCCEAFRFAVPKFTPNMLSVLDNLPGTKVAASEVERI 240
 DB 181 HDNIGSGNSESTQKCGIDVTLCCEAFRFAVPKFTPNMLSVLDNLPGTKVAASEVERI 240
 QY 241 KROHSSQEQTFQQLKMKQKNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLAME 300
 DB 241 KROHSSQEQTFQQLKMKQKNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLAME 300
 QY 301 SLPGKTVGAEDIEKTIKACKRPSDQILKLSLWRIRKNGDDTLKGLMALKHSKTYHFPKT 360
 DB 301 SLPGKTVGAEDIEKTIKACKRPSDQILKLSLWRIRKNGDDTLKGLMALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 RESULT 8
 ADD01625 standard; protein; 401 AA.
 AC ADD01625;
 XX
 DT 01-JAN-2004 (first entry)
 DE Human osteoprotegerin amino acid sequence SEQ ID NO:2.
 XX fibrotic disease; cysteine-rich domain; osteoprotegerin; scleroderma;
 KM antiinflammatory; gene therapy; human.
 XX Homo sapiens.
 OS
 PN WO2003084560-A2.
 PD 16-OCT-2003.
 PF 26-MAR-2003; 2003WO-EP050080.
 PR 10-APR-2002; 2002EP-00100364.
 PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 PI Power C, Plater-Zyberk C;

XX WPI; 2003-804248/75.
 DR N-PSDB; ADD01624.
 XX
 PT Use of a substance for the manufacture of a medicament for treating or
 XX preventing fibrotic disease.
 PS Claim 1; SEQ ID NO 2; 68bp; English.
 CC The present invention describes a substance which is useful for the
 CC manufacture of a medicament for treating or preventing fibrotic disease.
 CC The substance comprises: (a) a polypeptide comprising a fully defined
 CC sequence having 401 amino acids (see ADD01625 and ADD01627), or its amino
 CC acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4
 CC cysteine-rich domains of osteoprotegerin; (c) a mixture of (a)-(b) that is
 CC encoded by a DNA sequence that hybridises to the complement of the DNA
 CC sequence encoding (a)-(b) under moderately or highly stringent conditions
 CC ; where the amino acid sequence has at least 40, 50, 60, 70, 80 or 90%
 CC identity with (a)-(b); and where any changes in the amino acid sequence
 CC are conservative amino acid substitutions to the amino acid sequences in
 CC (a)-(b); or (d) a salt or an isoform, fused protein, functional
 CC derivative, active fraction or circularly permuted derivative of (a)-
 CC (c). Also described: (1) a polypeptide comprising the 401-amino acid
 CC sequence and one, two, three or four cysteine-rich domains of
 CC osteoprotegerin; and (2) a method for treating or preventing a fibrotic
 CC disease, particularly scleroderma. The substance has antiinflammatory
 CC activity, and can be used in gene therapy. A vector or cell comprising
 CC the nucleic acid molecule encoding a polypeptide of the invention can be
 CC used for inducing or enhancing the endogenous production of the
 CC polypeptide in a cell for the preparation of a medicament for treating or
 CC preventing a fibrotic disease, in particular scleroderma. The present
 CC sequence represents a human osteoprotegerin amino acid sequence which is
 CC used in the exemplification of the present invention.
 XX
 SQ Sequence 401 AA:
 Query Match 100.0%; Score 401; DB 7; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEBTSQQLCDKCPGTYLKQHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEBTSQQLCDKCPGTYLKQHTAKMKT 60
 QY 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNRTNHRVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNRTNHRVCEKGRYLEIEFCLK 120
 QY 121 HRSCPPGFGVQAQTPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 DB 121 HRSCPPGFGVQAQTPERNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNAT 180
 QY 181 HDNIGSGNSESTQKCGIDVTLCCEAFRFAVPKFTPNMLSVLDNLPGTKVAASEVERI 240
 DB 181 HDNIGSGNSESTQKCGIDVTLCCEAFRFAVPKFTPNMLSVLDNLPGTKVAASEVERI 240
 QY 241 KROHSSQEQTFQQLKMKQKNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLAME 300
 DB 241 KROHSSQEQTFQQLKMKQKNDIVKTIQDIDLCENSVQRIHGANLTFEQLSLAME 300
 QY 301 SLPGKTVGAEDIEKTIKACKRPSDQILKLSLWRIRKNGDDTLKGLMALKHSKTYHFPKT 360
 DB 301 SLPGKTVGAEDIEKTIKACKRPSDQILKLSLWRIRKNGDDTLKGLMALKHSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 RESULT 9
 AAR99925 standard; protein; 401 AA.
 ID AAR99925

AA99925;
 22-APR-1997 (first entry)
 Full length osteoclastogenesis inhibitory factor.
 Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
 osteoporosis.
 Homo sapiens.
 Key
 Peptide
 Protein
 Location/Qualifiers
 1..21
 /note= "Signal peptide"
 22..401
 /note= "Mature OCIF, claim 6"
 WO9626217-A1.
 29-AUG-1996.
 20-FEB-1996; 96WO-JP000374.
 20-FEB-1995; 95JP-00054977.
 21-JUL-1995; 95JP-00207508.
 (SNOW) SNOW BRAND MILK PROD CO LTD.
 Goto M, Tsuda E, Mochizuki S, Yano K, Kobayashi F, Shima N,
 Yasuda H, Nakagawa N, Morinaga T, Ueda M, Higashio K,
 WPI: 1996-402320/40.
 N-PSDB; AAT36685.
 DNA encoding osteoclastogenesis inhibitory factor protein - useful for
 bone resorption control, esp. treatment of osteoporosis.
 Disclosure; Page 64-66; 183pp; Japanese.
 This sequence represents the full length osteoclastogenesis inhibitory
 factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-
 PAGE of 60 kD under reducing conditions and 120 kD under non-reducing
 conditions. The protein is adsorbed onto cation-exchangers or heparin and
 its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C,
 and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of
 bone resorption and therefore in the treatment and prevention of
 disorders of bone resorption, e.g. osteoporosis
 Sequence 401 AA;
 Query Match 99.3%; Score 398; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 LILCALVFLDISIKMTQETFPKYLHYDETSQHLCDKCPRTYLYKQHTAKWKTVCA 63
 4 LILCALVFLDISIKMTQETFPKYLHYDETSQHLCDKCPRTYLYKQHTAKWKTVCA 63
 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLEIFCLKHS 123
 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLEIFCLKHS 123
 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLEIFCLKHS 123
 124 CPPEFGVYQAGTPRRNTYCKRCPRGFFSNETSSTAFCRKHTNGCVFGLLLTOKGNATHDN 183
 124 CPPEFGVYQAGTPRRNTYCKRCPRGFFSNETSSTAFCRKHTNGCVFGLLLTOKGNATHDN 183
 124 CPPEFGVYQAGTPRRNTYCKRCPRGFFSNETSSTAFCRKHTNGCVFGLLLTOKGNATHDN 183
 124 CPPEFGVYQAGTPRRNTYCKRCPRGFFSNETSSTAFCRKHTNGCVFGLLLTOKGNATHDN 183
 184 ICSGNSBSTOKCGIDVLTCEAFRFAVPTKFTNMILSVLVNDLPGTKVNAESYERIKRO 243
 184 ICSGNSBSTOKCGIDVLTCEAFRFAVPTKFTNMILSVLVNDLPGTKVNAESYERIKRO 243
 184 ICSGNSBSTOKCGIDVLTCEAFRFAVPTKFTNMILSVLVNDLPGTKVNAESYERIKRO 243
 244 HSSQEQTFQLLKMKQNKQDQIVKIIODIDLCEVNSVORHIGANTFEQLRSLMESLP 303
 244 HSSQEQTFQLLKMKQNKQDQIVKIIODIDLCEVNSVORHIGANTFEQLRSLMESLP 303

304 GKIVGADIETKTKACKPSDQILKLSLWRIKNGDDPTLKGIMHALKHSKTYHPKTVTQ 363
 304 GKIVGADIETKTKACKPSDQILKLSLWRIKNGDDPTLKGIMHALKHSKTYHPKTVTQ 363
 364 SLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 364 SLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 RESULT 10
 AAW53239
 ID AAW53239 standard; protein; 401 AA.
 XX
 AAW53239;
 15-JUL-1998 (first entry)
 Human OCIF genome DNA protein.
 Human OCIF genome DNA protein.
 Human; OCIF; genome; osteoclast; antipyretic; osteoporosis; rheumatism;
 multiple sclerosis.
 Homo sapiens.
 Key
 Peptide
 Protein
 Location/Qualifiers
 1..21
 /label= signal
 22..401
 /label= OCIF_protein
 WO9807840-A1.
 26-FEB-1998.
 19-AUG-1997; 97WO-JP002859.
 19-AUG-1996; 96JP-00235928.
 (SNOW) SNOW BRAND MILK PROD CO LTD.
 Nakagawa N, Yasuda H, Morinaga T;
 WPI: 1998-169150/15.
 N-PSDB; AAV20768.
 Inhibition of osteoclast formation and/or antipyretic activity - useful
 for, e.g. treating osteoporosis, rheumatism and multiple sclerosis.
 Claim 4; Page 26-28; 36pp; English.
 The present sequence represents human OCIF genome DNA protein which is
 specifically claimed in the present invention. The present invention
 describes: (1) a method of inhibiting the formation of osteoclasts and/or
 antipyretic proteins, which have the following characteristics: (i) MW
 determined by SDS-PAGE of approximately 60 kDa under reducing conditions,
 and 60 kDa and 120 kDa under non-reducing conditions; (ii) 401 aa
 sequence (iii) (see AAW53239); (iii) affinity to cation exchangers and
 heparin; (iv) its osteoclast formation inhibiting activity reduced by
 heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius for 30
 minutes, and (v) its antipyretic activity reduced by heating at 90
 degrees Celsius for 10 minutes, and (2) a method for preparing the above
 proteins. The proteins are useful for, e.g. treatment and prevention of
 osteoporosis, rheumatism or multiple sclerosis, and also as antigens for
 immunological diagnosis of these diseases and disorders
 Sequence 401 AA;
 Query Match 99.3%; Score 398; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 LILCALVFLDISIKMTQETFPKYLHYDETSQHLCDKCPRTYLYKQHTAKWKTVCA 63

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Db      4  LCCALVFLDISIKMTTQETFPFKYLHYDEBTSHQLLCDKCPPTGYLKQCHTAKMKTVCA 63
Qy      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Db      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Qy      124  CPDGFVQVAGTPERNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
Db      124  CPDGFVQVAGTPERNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
Qy      184  ICSGNESTQKCGIDVTLCCEAFPRFAVPTKFTPNMLSVLVNLPPTKVNAESVERIKRQ 243
Db      184  ICSGNESTQKCGIDVTLCCEAFPRFAVPTKFTPNMLSVLVNLPPTKVNAESVERIKRQ 243
Qy      244  HSSQEQTFQLLKLMKQKQNDIVKKIIDDICENSVRHIGHANLTPEQLRSLMESLP 303
Db      244  HSSQEQTFQLLKLMKQKQNDIVKKIIDDICENSVRHIGHANLTPEQLRSLMESLP 303
Qy      304  GKRVGAEDEIKTKKCKPSDOIILKLSLWIRKNGDDDTLKGMLHALKHSKTYHFPKTVQ 363
Db      304  GKRVGAEDEIKTKKCKPSDOIILKLSLWIRKNGDDDTLKGMLHALKHSKTYHFPKTVQ 363
Qy      364  SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db      364  SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

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RESULT 11
ID      AAY8622 standard; protein; 401 AA.
XX      AAY8622;
XX      18-AUG-2000 (first entry)
XX      Osteoclastogenesis inhibitory factor (OCIF) protein sequence.
XX      Osteoclastogenesis inhibitory factor; OCIF; cachexia; treatment; oedema;
XX      malignant tumour; tuberculosis; diabetes; blood disease; anorexia;
XX      endocrine disorder; infection; AIDS; weight loss; anaemia.
XX      Homo sapiens.
XX      OS
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      1..21
XX      FT      Protein      /label= Signal peptide
XX      FT      Protein      22..401
XX      FT      Protein      /label= Osteoclastogenesis inhibitory factor
XX      NO200021554-A1.
XX      20-APR-2000.
XX      PF      08-OCT-1999; 99WO-JP005570.
XX      PR      09-OCT-1998; 98JP-00287738.
XX      PA      (SANY ) SANKYO CO LTD.
XX      PA      (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX      PI      Oizumi K, Kurakata S;
XX      DR      WPI, 2000-317844/27.
XX      Novel compound containing osteoclastogenesis inhibitory factor active
XX      ingredient, for treating cachexia due to, e.g. malignant tumor,
XX      tuberculosis, diabetes and blood diseases.
XX      Claim 1; Page 9-10; 13pp; Japanese.
XX      This sequence represents the human osteoclastogenesis inhibitory factor
XX      (OCIF) amino acid sequence. OCIF is used in compounds for the treatment

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CC      of cachexia. The compounds are used for preventing or treating cachexia
CC      due to a malignant tumour, tuberculosis, diabetes, blood diseases,
CC      endocrine disorders, infections, AIDS, weight loss, anaemia, oedema, and
CC      anorexia
XX      SQ      Sequence 401 AA;
Qy      Query Match      99.3%; Score 398; DB 3; Length 401;
Qy      Best Local Similarity 100.0%; Pred. No. 0;
Qy      Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      4  LCCALVFLDISIKMTTQETFPFKYLHYDEBTSHQLLCDKCPPTGYLKQCHTAKMKTVCA 63
Qy      4  LCCALVFLDISIKMTTQETFPFKYLHYDEBTSHQLLCDKCPPTGYLKQCHTAKMKTVCA 63
Db      4  LCCALVFLDISIKMTTQETFPFKYLHYDEBTSHQLLCDKCPPTGYLKQCHTAKMKTVCA 63
Qy      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Db      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Qy      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Db      64  PCPDHYTDSWHTSDECLYCSPVCKELQYVQKQCNTRHNRCVCEKGRYLEIEFCLKHS 123
Qy      124  CPDGFVQVAGTPERNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
Db      124  CPDGFVQVAGTPERNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
Qy      184  ICSGNESTQKCGIDVTLCCEAFPRFAVPTKFTPNMLSVLVNLPPTKVNAESVERIKRQ 243
Db      184  ICSGNESTQKCGIDVTLCCEAFPRFAVPTKFTPNMLSVLVNLPPTKVNAESVERIKRQ 243
Qy      244  HSSQEQTFQLLKLMKQKQNDIVKKIIDDICENSVRHIGHANLTPEQLRSLMESLP 303
Db      244  HSSQEQTFQLLKLMKQKQNDIVKKIIDDICENSVRHIGHANLTPEQLRSLMESLP 303
Qy      304  GKRVGAEDEIKTKKCKPSDOIILKLSLWIRKNGDDDTLKGMLHALKHSKTYHFPKTVQ 363
Db      304  GKRVGAEDEIKTKKCKPSDOIILKLSLWIRKNGDDDTLKGMLHALKHSKTYHFPKTVQ 363
Qy      364  SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db      364  SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
RESULT 12
ID      ABP70997 standard; protein; 401 AA.
XX      ABP70997;
XX      06-AUG-2003 (first entry)
XX      Human osteoclastogenesis inhibitory factor, OCIF.
XX      Human; osteopathic; antiarthritic; cytosolic; antisticking;
XX      dermatological; immunomodulator; osteoporosis; osteopenia;
XX      osteoclastogenesis inhibitory factor; OCIF; bone metabolic disease;
XX      Paget's disease; osteomyelitis; hypercalcaemia; osteoclasts;
XX      joint destruction; rheumatism; osteoarthritis; cancer; osteonecrosis;
XX      Gaucher's disease; sickle cell anaemia; lupus erythematosus;
XX      osteodystrophy; cachexia.
XX      Homo sapiens.
XX      OS
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      1..21
XX      FT      Protein      /label= Signal peptide
XX      FT      Protein      22..401
XX      FT      Protein      /label= Mature_protein
XX      PN      EP1270015-A2.
XX      PD      02-JUN-2003.
XX      PF      26-JUN-2002; 2002EP-00254497.
XX      PR      29-JUN-2001; 2001JP-00198985.

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XX (SANY) SANKYO CO LTD.
 PA Yamamoto S, Okada J, Kurihara A, Numazawa T, Kondo J, Tsuda E;
 PI Mochizuki S, Nishi H, Miyazaki H;
 XX WPI; 2003-459564/44.
 DR
 XX
 PT Complex for manufacturing medicaments for prophylaxis or treatment of
 PT bone metabolic diseases e.g. osteoporosis or osteoarthritis, comprises
 PT osteoclastogenesis inhibitory factor is bound to a polysaccharide.
 PS
 XX Claim 5; Page 26-28; 31pp; English.
 XX
 CC The present invention relates to a complex (I) comprising
 CC osteoclastogenesis inhibitory factor (OCIF), or its analogs or variants,
 CC bound to a polysaccharide or its derivatives. The present sequence is
 CC human OCIF. (I) is useful for prolonging the time that OCIF or an analog
 CC or variant of it is retained in the bloodstream after administration to a
 CC patient, by complexing prior to administration an OCIF with a
 CC polysaccharide. (I) is useful for the manufacture of a medicament for the
 CC prophylaxis or treatment of bone metabolic diseases. The bone metabolic
 CC diseases include osteoporosis, osteopenia, Paget's disease,
 CC osteomyelitis, infectious focus due to loss of bone, hypercalcaemia,
 CC osteoclasts, joint destruction or osteopenia due to rheumatism,
 CC osteoarthritis, loss of periodontal bone, cancer metastasis of bone,
 CC osteonecrosis or osteocyte death accompanying traumatic injury, Gaucher's
 CC disease, sickle cell anaemia, lupus erythematosus, systemic or
 CC nontraumatic injury, osteodystrophy, and cachexia due to solid carcinoma
 CC or cancer metastasis of bone or haemology-malignant disease
 CC
 XX
 SQ Sequence 401 AA:
 Query Match 99.3%; Score 398; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 LCCALVFLDISIKMTQETPPKYLHYDEBTSQHLCDKCPPTGYLKQHTAKMKTVCA 63
 Db 4 LCCALVFLDISIKMTQETPPKYLHYDEBTSQHLCDKCPPTGYLKQHTAKMKTVCA 63
 Oy 64 PCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNHNVCCEKGRYLEIEFCLKGRS 123
 Db 64 PCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNHNVCCEKGRYLEIEFCLKGRS 123
 Oy 124 CPDGFVQVQAGTPERNVTCRCPCDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 183
 Db 124 CPDGFVQVQAGTPERNVTCRCPCDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 183
 Oy 184 ICSGNSBSTOKCGIDVTLCEAFAFRPAVPTKFTPMNLVVDNLPGTKVAESVERIKRQ 243
 Db 184 ICSGNSBSTOKCGIDVTLCEAFAFRPAVPTKFTPMNLVVDNLPGTKVAESVERIKRQ 243
 Oy 244 HSSQEQTFOLLKLMKQNKQODIVKKIIOIDIDLCENSQVQRIHGANLTFEQLSLMESLP 303
 Db 244 HSSQEQTFOLLKLMKQNKQODIVKKIIOIDIDLCENSQVQRIHGANLTFEQLSLMESLP 303
 Oy 304 GKRYGABDIETIKIACRPSDQILKLLSLMRIKNGQDOTLKGLMHAKSKSTYHPKTVQ 363
 Db 304 GKRYGABDIETIKIACRPSDQILKLLSLMRIKNGQDOTLKGLMHAKSKSTYHPKTVQ 363
 Oy 364 SLKKTIRPLHSFTMYKLYOKLFLFMIGNQVSVISCL 401
 Db 364 SLKKTIRPLHSFTMYKLYOKLFLFMIGNQVSVISCL 401
 RESULT 13
 ADD37427 standard; procein; 401 AA.
 XX ADD37427;
 AC
 XX
 DT 15-JAN-2004 (first entry)

XX Human osteoclastogenic inhibitory factor complex encoding sequence.
 DE
 XX
 KW osteoclastogenic inhibitory factor; OCIF; prostaglandin; osteopathic;
 KW Antirheumatic; Antiarthritic; Cytostatic; Immunosuppressive;
 KW Antiinflammatory; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 XX WO2003074084-A1.
 XX
 XX 12-SEP-2003.
 XX
 XX 27-FEB-2003; 2003WO-JP002259.
 XX
 XX 01-MAR-2002; 2002JP-0005356.
 PA (SANY) SANKYO CO LTD.
 XX
 XX Kunakura S, Nakajima T;
 PI
 XX WPI; 2003-853480/79.
 DR
 XX
 XX Composition containing complex of osteoclastogenic inhibitory factor and
 PT polysaccharide, useful for treating metabolic bone disease, also contains
 PT inhibitor of prostaglandin.
 PS
 XX Claim 8; SEQ ID NO 1; 93pp; English.
 XX
 CC The present invention relates to a complex of at least one
 CC osteoclastogenic inhibitory factor (OCIF), or its analog or variant,
 CC bonded to a polysaccharide and a substance that suppresses production of
 CC prostaglandin and/or completes with biological activity of prostaglandin.
 CC The complex is used to treat or prevent a wide range of metabolic bone
 CC diseases, specifically osteoporosis, osteopenia, Paget's disease,
 CC osteomyelitis, infectious foci due to bone loss, hypercalcaemia,
 CC osteoclasts, joint destruction caused by rheumatism, osteoarthritis, loss
 CC of periodontal bone, cancer metastasis to bone, osteonecrosis or
 CC osteocyte death caused by traumatic injury, Gaucher's disease, sickle
 CC cell anemia, systemic lupus erythematosus, non-traumatic injury,
 CC osteodystrophy and cachexia caused by carcinoma, metastasis or malignant
 CC blood diseases. Administration of OCIF as a complex ensures prolonged
 CC retention in the circulation, while co-administration with the complex
 CC results in a synergistic increase in activity. The present sequence
 CC represents human osteoclastogenic inhibitory factor complex encoding
 CC sequence.
 CC
 XX
 SQ Sequence 401 AA:
 Query Match 99.3%; Score 398; DB 7; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 LCCALVFLDISIKMTQETPPKYLHYDEBTSQHLCDKCPPTGYLKQHTAKMKTVCA 63
 Db 4 LCCALVFLDISIKMTQETPPKYLHYDEBTSQHLCDKCPPTGYLKQHTAKMKTVCA 63
 Oy 64 PCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNHNVCCEKGRYLEIEFCLKGRS 123
 Db 64 PCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNHNVCCEKGRYLEIEFCLKGRS 123
 Oy 124 CPDGFVQVQAGTPERNVTCRCPCDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 183
 Db 124 CPDGFVQVQAGTPERNVTCRCPCDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 183
 Oy 184 ICSGNSBSTOKCGIDVTLCEAFAFRPAVPTKFTPMNLVVDNLPGTKVAESVERIKRQ 243
 Db 184 ICSGNSBSTOKCGIDVTLCEAFAFRPAVPTKFTPMNLVVDNLPGTKVAESVERIKRQ 243
 Oy 244 HSSQEQTFOLLKLMKQNKQODIVKKIIOIDIDLCENSQVQRIHGANLTFEQLSLMESLP 303
 Db 244 HSSQEQTFOLLKLMKQNKQODIVKKIIOIDIDLCENSQVQRIHGANLTFEQLSLMESLP 303

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Qy 304 GKRVGADIEKTIKACKPSDQILKLSLWRIRKNGDDDTLKGMLHALKSKTYHFPKTVQ 363
Db 304 GKRVGADIEKTIKACKPSDQILKLSLWRIRKNGDDDTLKGMLHALKSKTYHFPKTVQ 363
Qy 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 14
AAR99942
ID AAR99942 standard; protein; 399 AA.
AC AAR99942;
XX
XX
DT 23-APR-1997 (first entry)
XX
XX Mutated OCIF, OCIF-CL.
DE
XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KM osteoporosis.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /note="Signal peptide"
FT Protein 22..399
FT /note="Mature OCIF-CL"
XX
XX MO626217-A1.
PN 29-AUG-1996.
XX
XX 20-FEB-1996; 96MO-JP000374.
XX
XX 20-FEB-1995; 95JP-00054977.
PR 21-JUL-1995; 95JP-00207508.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA Goto M, Tsuda E, Mochizuki S, Yano K, Kobayashi F, Shima N;
PI Yasuda H, Nakagawa N, Morinaga T, Ueda M, Higashio K;
PI
XX WPI; 1996-402320/40.
DR N-PSDB; AAT33172.
XX
XX DNA encoding osteoclastogenesis inhibitory factor protein - useful for
PT bone resorption control, esp. treatment of osteoporosis.
XX
XX Claim 62; Page 117-119; 183pp; Japanese.
XX
XX This sequence represents a mutated version of the full length
CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC sequence represents OCIF-CL in which amino acids 379-380 of the mature
CC OCIF protein are deleted. The OCIF of the invention has a molecular
CC weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
CC mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
CC in the control of bone resorption and therefore in the treatment and
CC prevention of disorders of bone resorption, e.g. osteoporosis
XX
XX Sequence 399 AA;
SO

Query Match 98.8%; Score 396; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LCCALVFLDISIKWTQETFPKRYLHYDEBTSQQLCDKCPRTYKQCHTAKWTVCA 63
Db 4 LCCALVFLDISIKWTQETFPKRYLHYDEBTSQQLCDKCPRTYKQCHTAKWTVCA 63

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Qy 64 PCPDHYTDSWHTSDECLYCSFVCKELQYVKQECNRTHNRVCECKGRYLEIEFCLKHRS 123
Db 64 PCPDHYTDSWHTSDECLYCSFVCKELQYVKQECNRTHNRVCECKGRYLEIEFCLKHRS 123
Qy 124 CPFGFVVOAGTPERNTVCKRCPDGFFSNETSCKAPCRGHTNCSVFGLLLTQKGNATHDN 183
Db 124 CPFGFVVOAGTPERNTVCKRCPDGFFSNETSCKAPCRGHTNCSVFGLLLTQKGNATHDN 183
Qy 184 ICSGNESTQKCGIDVTLCEBAFPFPAVPTKFTPMVLSTLVNLPCTKYNAASVERIKRQ 243
Db 184 ICSGNESTQKCGIDVTLCEBAFPFPAVPTKFTPMVLSTLVNLPCTKYNAASVERIKRQ 243
Qy 244 HSSQEQTFQLKLMKQKQNDQIVKKIIDDLCENSVGRHIGHANLTPEQRLSMEISLP 303
Db 244 HSSQEQTFQLKLMKQKQNDQIVKKIIDDLCENSVGRHIGHANLTPEQRLSMEISLP 303
Qy 304 GKRVGADIEKTIKACKPSDQILKLSLWRIRKNGDDDTLKGMLHALKSKTYHFPKTVQ 363
Db 304 GKRVGADIEKTIKACKPSDQILKLSLWRIRKNGDDDTLKGMLHALKSKTYHFPKTVQ 363
Qy 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKIS 399
Db 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKIS 399

```

```

RESULT 15
AAM53238
ID AAM53238 standard; protein; 391 AA.
XX
XX AAM53238;
AC
XX
XX 15-JUL-1998 (first entry)
DT
XX
XX Human OCIF genome DNA-2 protein.
DE
XX
XX Human; OCIF; genome; osteoclast; antipyretic; osteoporosis; rheumatism;
KW multiple sclerosis.
XX
XX Homo sapiens.
OS
XX
XX MO9807840-A1.
PN 26-FEB-1998.
XX
XX 19-AUG-1997; 97MO-JP002859.
PF
XX 19-AUG-1996; 96JP-00235928.
PR
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA Nakagawa N, Yasuda H, Morinaga T;
PI
XX WPI; 1998-169150/15.
DR N-PSDB; AAV20767.
XX
XX Inhibition of osteoclast formation and/or antipyretic activity - useful
PT for, e.g. treating osteoporosis, rheumatism and multiple sclerosis.
XX
XX Disclosure; Page 16-26; 36pp; English.
XX
XX The present sequence represents human OCIF genome DNA protein which is
CC shown in the present invention. The present invention describes: (i) a
CC method of inhibiting the formation of osteoclasts and/or antipyretic
CC proteins, which have the following characteristics: (i) MW determined by
CC SDS-PAGE of approximately 60 kDa under reducing conditions, and 60 kDa
CC and 120 kDa under non-reducing conditions; (ii) 401 aa sequence (iii) its
CC (see AAM53339); (iii) affinity to cation exchangers and heparin; (iv) its
CC osteoclast formation inhibiting activity reduced by heating at 70 degrees
CC Celsius for 10 minutes or 56 degrees Celsius for 30 minutes, and (v) its
CC antipyretic activity reduced by heating at 90 degrees Celsius for 10
CC minutes, and (2) a method for preparing the above proteins. The proteins
CC are useful for; e.g. treatment and prevention of osteoporosis, rheumatism
CC or multiple sclerosis, and also as antigens for immunological diagnosis

```


CC of these diseases and disorders
 XX
 SQ Sequence 391 AA;

Query Match 97.5%; Score 391; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	FLDISIKKWTTOETFPFKYLIHYDEETSHQLLCDKCPPTGYLKHQCTAKMKTVCAPCPDHY	60
QY	71	TDSMHTSDECLYCSPVCKELOYVVKQECNRTHNRVCECKEGRYLIEFCLKHRSCTPGFGV	130
DB	61	TDSMHTSDECLYCSPVCKELOYVVKQECNRTHNRVCECKEGRYLIEFCLKHRSCTPGFGV	120
QY	131	VOAGTPEBNTVCRCPCPDGFFSNSTSSKAPCRKHTNCVFGLLLTQKGNATHDNICSGNSE	190
DB	121	VOAGTPEBNTVCRCPCPDGFFSNSTSSKAPCRKHTNCVFGLLLTQKGNATHDNICSGNSE	180
QY	191	STOKGIDVTLCEEAFFRPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSQEQ	250
DB	181	STOKGIDVTLCEEAFFRPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSQEQ	240
QY	251	FOLKLMKHONKODIVKKIIDDIDLCENSVORHIGHANLTPBOLRLMESLPGKKVGA	310
DB	241	FOLKLMKHONKODIVKKIIDDIDLCENSVORHIGHANLTPBOLRLMESLPGKKVGA	300
QY	311	DIEKTIKACKPSDQILKLSLWRIKNGDQDTLKGIMHALKHSKTYHPPKTVTOSLAKTIR	370
DB	301	DIEKTIKACKPSDQILKLSLWRIKNGDQDTLKGIMHALKHSKTYHPPKTVTOSLAKTIR	360
QY	371	FLHSTMYKLYOKLFLEMIIGNOVQSVKISCL	401
DB	361	FLHSTMYKLYOKLFLEMIIGNOVQSVKISCL	391

Search completed: September 29, 2004, 12:47:56
 Job time : 129 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 12:50:39 ; Search time 134 Seconds

(without alignments)
962.996 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 401

Sequence: 1 MNKLCCALVFLDISIKMTT.....OKLFLEMIGNVQSVKISCL 401

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1351062 seqs, 321799191 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2427

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	100.0	401	12	US-10-105-934-2
2	401	100.0	401	13	US-10-039-785-5
3	401	100.0	401	13	US-10-066-309-1
4	401	100.0	401	13	US-10-164-592-2
5	401	100.0	401	14	US-10-044-674-3
6	401	100.0	401	14	US-10-332-673-5
7	401	100.0	401	14	US-10-139-785-5
8	398	99.3	401	9	US-09-062-113-5
9	398	99.3	401	14	US-10-183-091-1
10	398	99.3	401	14	US-10-364-045-1
11	398	99.3	401	14	US-10-232-858-5
12	398	99.3	401	15	US-10-377-076-1
13	398	99.3	401	16	US-10-785-109-5
14	398	99.3	401	16	US-10-785-114-5
15	396	98.8	399	9	US-09-062-113-73

16	396	98.8	399	14	US-10-232-858-73	Sequence 73, Appl
17	396	98.8	399	16	US-10-785-109-73	Sequence 73, Appl
18	396	98.8	399	16	US-10-785-114-73	Sequence 73, Appl
19	396	98.8	401	9	US-09-062-113-66	Sequence 66, Appl
20	396	98.8	401	14	US-10-232-858-66	Sequence 66, Appl
21	396	98.8	401	16	US-10-785-109-66	Sequence 66, Appl
22	396	98.8	401	16	US-10-785-114-66	Sequence 66, Appl
23	391	97.5	391	9	US-09-062-113-106	Sequence 106, App
24	391	97.5	391	14	US-10-232-858-106	Sequence 106, App
25	391	97.5	391	16	US-10-785-109-106	Sequence 106, App
26	391	97.5	391	16	US-10-785-114-106	Sequence 106, App
27	388	96.8	393	9	US-09-062-113-79	Sequence 79, Appl
28	388	96.8	393	14	US-10-232-858-79	Sequence 79, Appl
29	388	96.8	393	16	US-10-785-109-79	Sequence 79, Appl
30	388	96.8	393	16	US-10-785-114-79	Sequence 79, Appl
31	380	94.8	380	9	US-09-062-113-4	Sequence 4, Appl1
32	380	94.8	380	14	US-10-232-858-4	Sequence 4, Appl1
33	380	94.8	380	16	US-10-785-109-4	Sequence 4, Appl1
34	380	94.8	380	16	US-10-785-114-4	Sequence 4, Appl1
35	358	89.3	390	14	US-10-155-167-2	Sequence 2, Appl1
36	348	86.8	351	9	US-09-062-113-74	Sequence 74, Appl
37	348	86.8	351	14	US-10-232-858-74	Sequence 74, Appl
38	348	86.8	351	16	US-10-785-109-74	Sequence 74, Appl
39	348	86.8	351	16	US-10-785-114-74	Sequence 74, Appl
40	338	84.3	360	9	US-09-062-113-67	Sequence 67, Appl
41	338	84.3	360	14	US-10-232-858-67	Sequence 67, Appl
42	338	84.3	360	16	US-10-785-109-67	Sequence 67, Appl
43	338	84.3	360	16	US-10-785-114-67	Sequence 67, Appl
44	315	78.6	321	9	US-09-062-113-80	Sequence 80, Appl
45	315	78.6	321	14	US-10-232-858-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-10-105-934-2
Sequence 2, Application US/10105934
Publication No. US20020150988A1

GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
Holtzman, Douglas
TITLE OF INVENTION: NOVEL MOLECULES OF THE PTMMA-070-
RELATED PROTEIN FAMILY AND THE T85-RELATED PROTEIN
FAMILY AND USES THEREOF

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/105,934
FILING DATE: 25-Mar-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/062,389
FILING DATE: 17-Apr-1998
APPLICATION NUMBER: 60/062,017
FILING DATE: 10-Oct-1997
APPLICATION NUMBER: 60/044,746
FILING DATE: 18-Apr-1997

ATTORNEY/AGENT INFORMATION:
NAME: Melkejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/051001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-105-934-2

Query Match 100.0%; Score 401; DB 12; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETPPPKYLHYDEBTSQHLCDKCPGTYLKQHCSTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTQETPPPKYLHYDEBTSQHLCDKCPGTYLKQHCSTAKMKT 60
 QY 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKECNRTNHRVCECKEGRYLEIEFCUK 120
 DB 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKECNRTNHRVCECKEGRYLEIEFCUK 120
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 DB 121 HRSCEPFGVQAQTPERTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180
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 DB 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRFVPTKFTPNMLSVLVNLPGTKVAESVERI 240
 QY 241 KROHSQEQTFQKLKMKHQNKDQIVKTIIDIDLCENSVORHIGHANLTFEQLSLME 300
 DB 241 KROHSQEQTFQKLKMKHQNKDQIVKTIIDIDLCENSVORHIGHANLTFEQLSLME 300
 QY 301 SLPGKVGAEDEIKTIKACKPSDQILKLSLWRIKNGDDTLKGLMHALKSHKTYHFPKT 360
 DB 301 SLPGKVGAEDEIKTIKACKPSDQILKLSLWRIKNGDDTLKGLMHALKSHKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2
 US-10-039-785-5
 ; Sequence 5, Application US/10039785
 ; Publication No. US20020067646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saicedo et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
 ; FILE REFERENCE: PF550
 ; CURRENT APPLICATION NUMBER: US/10/039, 785
 ; PRIOR FILING DATE: 2002-05-07
 ; PRIOR APPLICATION NUMBER: 60/369,860
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/341,237
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 60/331,310
 ; PRIOR FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,044
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: 60/327,364
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/323,807
 ; PRIOR FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/309,176
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/294,981
 ; PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/293,473
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
 LENGTH: 401
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-039-785-5

Query Match 100.0%; Score 401; DB 13; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MNKLCCALVFLDISIKMTTQETPPPKYLHYDEBTSQHLCDKCPGTYLKQHCSTAKMKT 60
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 DB 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKECNRTNHRVCECKEGRYLEIEFCUK 120
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 DB 121 HRSCEPFGVQAQTPERTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNAT 180
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 DB 181 HDNIGSGNSESTQKCGIDVTLCBEAFPRFVPTKFTPNMLSVLVNLPGTKVAESVERI 240
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 DB 301 SLPGKVGAEDEIKTIKACKPSDQILKLSLWRIKNGDDTLKGLMHALKSHKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3
 US-10-066-209-1
 ; Sequence 1, Application US/10066209
 ; Publication No. US20020115110A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brigham-Burke, Michael R.
 ; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
 ; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
 ; FILE REFERENCE: GH-50030-D1
 ; CURRENT APPLICATION NUMBER: US/10/066,209
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: 09/072,993
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/055,513
 ; PRIOR FILING DATE: 1997-08-13
 ; PRIOR APPLICATION NUMBER: 60/056,980
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/057,550
 ; PRIOR FILING DATE: 1997-08-29
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; US-10-066-209-1

Query Match 100.0%; Score 401; DB 13; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBTSNOLCDKCPGTYLKQHTAKMT 60
Db 1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBTSNOLCDKCPGTYLKQHTAKMT 60

Qy 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLIEFCLK 120
Db 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLIEFCLK 120

Qy 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
Db 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180

Qy 181 HDNICSNGSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSLVVNDLPGTKVNASVERI 240
Db 181 HDNICSNGSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSLVVNDLPGTKVNASVERI 240

Qy 240 VQSLKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 240 VQSLKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 4
US-10-164-592-2
; Sequence 2, Application US/10164592
; Publication No. US20020150989A1
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Fleischmann, Robert D.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 1488.071007
; CURRENT APPLICATION NUMBER: US/10/164,592
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 08/469,637
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US95/03216
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-592-2

Query Match 100.0%; Score 401; DB 13; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 KROHSSOEOTFOLKLMKHQKNDQDIYKKIIOIDILCENSVO RHIGHANLTFEOLRSIME 300
Db 241 KROHSSOEOTFOLKLMKHQKNDQDIYKKIIOIDILCENSVO RHIGHANLTFEOLRSIME 300

Qy 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLMRINKGDDTLKGLMHALKSKSTYHPKPT 360
Db 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLMRINKGDDTLKGLMHALKSKSTYHPKPT 360

Qy 361 VTOSLAKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTOSLAKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 5
US-10-044-674-3
; Sequence 3, Application US/10044674
; Publication No. US20030175710A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE TNFRSF11B GENE
; FILE REFERENCE: TNFRSF11B.MMH-0001US (CIP)
; CURRENT APPLICATION NUMBER: US/10/044,674
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/18803
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-674-3

Query Match 100.0%; Score 401; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBTSNOLCDKCPGTYLKQHTAKMT 60
Db 1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBTSNOLCDKCPGTYLKQHTAKMT 60

Qy 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLIEFCLK 120
Db 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQECNRTNRYCECKEGRYLIEFCLK 120

Qy 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
Db 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180

Qy 181 HDNICSNGSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSLVVNDLPGTKVNASVERI 240
Db 181 HDNICSNGSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSLVVNDLPGTKVNASVERI 240

Qy 241 KROHSSOEOTFOLKLMKHQKNDQDIYKKIIOIDILCENSVO RHIGHANLTFEOLRSIME 300
Db 241 KROHSSOEOTFOLKLMKHQKNDQDIYKKIIOIDILCENSVO RHIGHANLTFEOLRSIME 300

Qy 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLMRINKGDDTLKGLMHALKSKSTYHPKPT 360
Db 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLMRINKGDDTLKGLMHALKSKSTYHPKPT 360

Qy 361 VTOSLAKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTOSLAKTIIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 6
US-10-322-673-5

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; Sequence 5, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-5
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Query Match      100.0%; Score 401; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MNKLCCALVFLDISIKMTTOETPPPKYLHYDEETSHQLLDCDKCPGGTYLKQHCIAKMT 60
DB      1 MNKLCCALVFLDISIKMTTOETPPPKYLHYDEETSHQLLDCDKCPGGTYLKQHCIAKMT 60
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DB      61 VCACPDHYTYSWHTSDCLYCSPVCKELQYVKQECNTHNRVCEKGRYLEIEFCLK 120
QY      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      181 HDNCSGNSBSTQKCGIDVTLCCEAFPRFPAVPTKFTPNMLSVLVNLPGTKVAASVERI 240
DB      181 HDNCSGNSBSTQKCGIDVTLCCEAFPRFPAVPTKFTPNMLSVLVNLPGTKVAASVERI 240
QY      241 KROHSSQEOFTQFLKLMKHQKQDQIVKKIIOIDILCENSVOHIGHANLTFEQLRSIME 300
DB      241 KROHSSQEOFTQFLKLMKHQKQDQIVKKIIOIDILCENSVOHIGHANLTFEQLRSIME 300
QY      301 SLPGKTVGAEDIEKTIKACRPSDQILKLSLWRINKGDQDTLKGMLHAKHSTYHFPKT 360
DB      301 SLPGKTVGAEDIEKTIKACRPSDQILKLSLWRINKGDQDTLKGMLHAKHSTYHFPKT 360
QY      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
DB      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
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RESULT 7
US-10-139-785-5
; Sequence 5, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
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; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-5
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Query Match      100.0%; Score 401; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MNKLCCALVFLDISIKMTTOETPPPKYLHYDEETSHQLLDCDKCPGGTYLKQHCIAKMT 60
DB      1 MNKLCCALVFLDISIKMTTOETPPPKYLHYDEETSHQLLDCDKCPGGTYLKQHCIAKMT 60
QY      61 VCACPDHYTYSWHTSDCLYCSPVCKELQYVKQECNTHNRVCEKGRYLEIEFCLK 120
DB      61 VCACPDHYTYSWHTSDCLYCSPVCKELQYVKQECNTHNRVCEKGRYLEIEFCLK 120
QY      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB      121 HRSRPPGFVQAGTBERNTVCRCPCDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY      181 HDNCSGNSBSTQKCGIDVTLCCEAFPRFPAVPTKFTPNMLSVLVNLPGTKVAASVERI 240
DB      181 HDNCSGNSBSTQKCGIDVTLCCEAFPRFPAVPTKFTPNMLSVLVNLPGTKVAASVERI 240
QY      241 KROHSSQEOFTQFLKLMKHQKQDQIVKKIIOIDILCENSVOHIGHANLTFEQLRSIME 300
DB      241 KROHSSQEOFTQFLKLMKHQKQDQIVKKIIOIDILCENSVOHIGHANLTFEQLRSIME 300
QY      301 SLPGKTVGAEDIEKTIKACRPSDQILKLSLWRINKGDQDTLKGMLHAKHSTYHFPKT 360
DB      301 SLPGKTVGAEDIEKTIKACRPSDQILKLSLWRINKGDQDTLKGMLHAKHSTYHFPKT 360
QY      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
DB      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
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RESULT 8
US-09-062-113-5
; Sequence 5, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eiuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
```

```

APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
TITLE OF INVENTION: The Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESS: Teate, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062.113
FILING DATE: 17-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..380
OTHER INFORMATION: /note= "(OCIF protein)"
FEATURE:
NAME/KEY: Peptide
LOCATION: -21..0
OTHER INFORMATION: /note= "(signal peptide)"
US-09-062-113-5

Query Match          99.3%; Score 398; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 184 ICSGNSSTQKCGIDVTLCEBAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQ 243
OY 244 HSSQEQTFQILKMKHONKODIVKTIIDIDLCENSVQRHIGANTTFEQLRLMESLP 303
DB 244 HSSQEQTFQILKMKHONKODIVKTIIDIDLCENSVQRHIGANTTFEQLRLMESLP 303
OY 304 GKXVGADIEKTIKACRPSDILKLSLWRIKNGDDTLGLMALHRSKTYHFPKTYVQ 363
DB 304 GKXVGADIEKTIKACRPSDILKLSLWRIKNGDDTLGLMALHRSKTYHFPKTYVQ 363
OY 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQVXISCL 401
DB 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQVXISCL 401

RESULT 9
US-10-183-091-1
Sequence 1, Application US/10183091
Publication No. US20030045456A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Shinichi
APPLICANT: Okada, Junichi
APPLICANT: Kurihara, Atsushi
APPLICANT: Numazawa, Taku
APPLICANT: Kondo, Junichi Tsuda, Eisuke
APPLICANT: Mochizuki, Shinichi
APPLICANT: Nishi, Hirotaka
TITLE OF INVENTION: A complex comprising OCIF and polyeaccharide
FILE REFERENCE: 02280/HG
CURRENT APPLICATION NUMBER: US/10/183,091
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: JP 2001-198985
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (-21)..(-1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (+1)..(+380)
OTHER INFORMATION:
US-10-183-091-1

Query Match          99.3%; Score 398; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 244 HSSGEOTFOLLKLMKQKODIVKKI IODIDLCEMSVORHIGHANLTFEQLSLMESLP 303
QY 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363
Db 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363
QY 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 10
US-10-364-045-1
; Sequence 1, Application US/10364045
; Publication No. US2003013325A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Shinichi
; APPLICANT: Okada, Junichi
; APPLICANT: Kurihara, Atsushi
; APPLICANT: Numazawa, Taku
; APPLICANT: Kondo, Junichi Tsuda, Eisuke
; APPLICANT: Mochizuki, Shinichi
; APPLICANT: Nishi, Hirotaka
; APPLICANT: Miyazaki, Hideki
; TITLE OF INVENTION: A complex comprising OCIF and polysaccharide
; FILE REFERENCE: 02280/HG
; CURRENT APPLICATION NUMBER: US/10/364,045
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US/10/183,091
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: JP 2001-198985
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (-21)..(-1)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (+1)..(+380)
; OTHER INFORMATION:
US-10-364-045-1

Query Match 99.3%; Score 398; DB 14; Length 401;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LILCALVFLDISIKMTTOETPPRYLHYDETSHQLCDKCPRTYIKOHTAKMTVCA 63
Db 4 LILCALVFLDISIKMTTOETPPRYLHYDETSHQLCDKCPRTYIKOHTAKMTVCA 63
QY 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEIFCLKHS 123
Db 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEIFCLKHS 123
QY 124 CPDGFVVOAGTPRNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNATHN 183
Db 124 CPDGFVVOAGTPRNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNATHN 183
QY 184 ICSGNSBSTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPPTKNAESVERIKRQ 243
Db 184 ICSGNSBSTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPPTKNAESVERIKRQ 243
QY 244 HSSGEOTFOLLKLMKQKODIVKKI IODIDLCEMSVORHIGHANLTFEQLSLMESLP 303
Db 244 HSSGEOTFOLLKLMKQKODIVKKI IODIDLCEMSVORHIGHANLTFEQLSLMESLP 303
QY 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363

Db 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363
QY 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 11
US-10-232-858-5
; Sequence 5, Application US/10232858
; Publication No. US20030153048A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20030153048A1uyuki
; APPLICANT: YASUDA, Hirotaka
; APPLICANT: NAKAGAWA, No. US20030153048A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masaeugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20030153048A1e1 Proteins and Methods for Producing the Prote
; FILE REFERENCE: 16991.004
; CURRENT APPLICATION NUMBER: US/10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: PCT/J996/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: 08/915,004
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-858-5

Query Match 99.3%; Score 398; DB 14; Length 401;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LILCALVFLDISIKMTTOETPPRYLHYDETSHQLCDKCPRTYIKOHTAKMTVCA 63
Db 4 LILCALVFLDISIKMTTOETPPRYLHYDETSHQLCDKCPRTYIKOHTAKMTVCA 63
QY 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEIFCLKHS 123
Db 64 PCPDHYTDSWHTSDECLYCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEIFCLKHS 123
QY 124 CPDGFVVOAGTPRNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNATHN 183
Db 124 CPDGFVVOAGTPRNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNATHN 183
QY 184 ICSGNSBSTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPPTKNAESVERIKRQ 243
Db 184 ICSGNSBSTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPPTKNAESVERIKRQ 243
QY 244 HSSGEOTFOLLKLMKQKODIVKKI IODIDLCEMSVORHIGHANLTFEQLSLMESLP 303
Db 244 HSSGEOTFOLLKLMKQKODIVKKI IODIDLCEMSVORHIGHANLTFEQLSLMESLP 303
QY 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363
Db 304 GKXVGADEIEKTIKACKPSDOIILKLSLWIRKNGDODTLKGLMHALKSHSTYHFPKTVQ 363
QY 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
Db 364 SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 12
US-10-377-076-1
; Sequence 1, Application US/10377076
; Publication No. US20030216297A1
; GENERAL INFORMATION:
; APPLICANT: Kumakura, Seichiro
; APPLICANT: Nakajima, Tomoko
; TITLE OF INVENTION: A Pharmaceutical Composition
; FILE REFERENCE: 03117/HG
; CURRENT APPLICATION NUMBER: US/10/377,076
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: JP 2002-055356
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (-21)..(-1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (+1)..(+380)
; OTHER INFORMATION:
US-10-377-076-1

Query Match 99.3%; Score 398; DB 15; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LILCALVFLDISIKMTTOETPPKYLHYDEETSHQLCDKCPGGTYLKQHTAKKTVCA 63
DB 4 LILCALVFLDISIKMTTOETPPKYLHYDEETSHQLCDKCPGGTYLKQHTAKKTVCA 63
QY 64 PCPDHYTDSWHTSECLCYSPVCKELOYVQECNRTNRCVCEKEGRLYEIEFLKHS 123
DB 64 PCPDHYTDSWHTSECLCYSPVCKELOYVQECNRTNRCVCEKEGRLYEIEFLKHS 123
QY 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 184 ICSGSESTQKCGIDVTLCEAFAFRFAVPTKFTPMWLSVLDNLPRTVNAESVERIKRQ 243
DB 184 ICSGSESTQKCGIDVTLCEAFAFRFAVPTKFTPMWLSVLDNLPRTVNAESVERIKRQ 243
QY 244 HSSQOTQOLKLMWQKQKDDIYKTIIDIDLCNSVQRIHGHANLTFEQLRSIMESLP 303
DB 244 HSSQOTQOLKLMWQKQKDDIYKTIIDIDLCNSVQRIHGHANLTFEQLRSIMESLP 303
QY 304 GKVGAEIDIEKTIKACRPSDQILKLLSLMRIKNGDDDTLKGMLALKHSKTYHFPKTVQ 363
DB 304 GKVGAEIDIEKTIKACRPSDQILKLLSLMRIKNGDDDTLKGMLALKHSKTYHFPKTVQ 363
QY 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
DB 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 13
US-10-785-109-5
; Sequence 5, Application US/10785109
; Publication No. US20040142426A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eiuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki

; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.017
; CURRENT APPLICATION NUMBER: US/10/785,109
; PRIOR FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-109-5

Query Match 99.3%; Score 398; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LILCALVFLDISIKMTTOETPPKYLHYDEETSHQLCDKCPGGTYLKQHTAKKTVCA 63
DB 4 LILCALVFLDISIKMTTOETPPKYLHYDEETSHQLCDKCPGGTYLKQHTAKKTVCA 63
QY 64 PCPDHYTDSWHTSECLCYSPVCKELOYVQECNRTNRCVCEKEGRLYEIEFLKHS 123
DB 64 PCPDHYTDSWHTSECLCYSPVCKELOYVQECNRTNRCVCEKEGRLYEIEFLKHS 123
QY 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPFGGVVQAGTPRNTVCKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 184 ICSGSESTQKCGIDVTLCEAFAFRFAVPTKFTPMWLSVLDNLPRTVNAESVERIKRQ 243
DB 184 ICSGSESTQKCGIDVTLCEAFAFRFAVPTKFTPMWLSVLDNLPRTVNAESVERIKRQ 243
QY 244 HSSQOTQOLKLMWQKQKDDIYKTIIDIDLCNSVQRIHGHANLTFEQLRSIMESLP 303
DB 244 HSSQOTQOLKLMWQKQKDDIYKTIIDIDLCNSVQRIHGHANLTFEQLRSIMESLP 303
QY 304 GKVGAEIDIEKTIKACRPSDQILKLLSLMRIKNGDDDTLKGMLALKHSKTYHFPKTVQ 363
DB 304 GKVGAEIDIEKTIKACRPSDQILKLLSLMRIKNGDDDTLKGMLALKHSKTYHFPKTVQ 363
QY 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
DB 364 SLKTIIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 14
US-10-785-114-5
; Sequence 5, Application US/10785114
; Publication No. US20040143859A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eiuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki

```

; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.016
; CURRENT APPLICATION NUMBER: US/10/785,114
; PRIOR FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-114-5

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Query Match          99.3%; Score 398; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 LCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGGTYLKQHTAKMTVCA 63
DB 4 LCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGGTYLKQHTAKMTVCA 63
QY 64 PCPDHYTDSWHTSDCLYCSPVCKELQYVVKQECNRTNHRVCECKEGRYLEIFCLKHS 123
DB 64 PCPDHYTDSWHTSDCLYCSPVCKELQYVVKQECNRTNHRVCECKEGRYLEIFCLKHS 123
QY 124 CPPEFGVQAGTPERNITVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPPEFGVQAGTPERNITVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 184 ICSGNSSESTQKCGIDVTLCEBAFFRAVPTKFTNNLSVLYDNLPGTKNAESVERIKRQ 243
DB 184 ICSGNSSESTQKCGIDVTLCEBAFFRAVPTKFTNNLSVLYDNLPGTKNAESVERIKRQ 243
QY 244 HSSQEQTFQLKMKHQNKKDDIVKTIIDIDLCNSVQRIHGANLTFEQLNSLMSLP 303
DB 244 HSSQEQTFQLKMKHQNKKDDIVKTIIDIDLCNSVQRIHGANLTFEQLNSLMSLP 303
QY 304 GKRVGADIEKTIKACRPSDQILKLSLWRILKNGDDDTLKGMLALGHSKTYHPKTVQ 363
DB 304 GKRVGADIEKTIKACRPSDQILKLSLWRILKNGDDDTLKGMLALGHSKTYHPKTVQ 363
QY 364 SLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401
DB 364 SLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401

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RESULT 15
US-09-062-113-73
; Sequence 73, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu

```

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; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1e1 Proteins and Methods for Producing
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: RJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -21..0
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..378
; OTHER INFORMATION: /note= "OCIF-CL"
US-09-062-113-73

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Query Match          98.8%; Score 396; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 LCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGGTYLKQHTAKMTVCA 63
DB 4 LCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGGTYLKQHTAKMTVCA 63
QY 64 PCPDHYTDSWHTSDCLYCSPVCKELQYVVKQECNRTNHRVCECKEGRYLEIFCLKHS 123
DB 64 PCPDHYTDSWHTSDCLYCSPVCKELQYVVKQECNRTNHRVCECKEGRYLEIFCLKHS 123
QY 124 CPPEFGVQAGTPERNITVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDN 183
DB 124 CPPEFGVQAGTPERNITVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLLTQKGNATHDN 183
QY 184 ICSGNSSESTQKCGIDVTLCEBAFFRAVPTKFTNNLSVLYDNLPGTKNAESVERIKRQ 243
DB 184 ICSGNSSESTQKCGIDVTLCEBAFFRAVPTKFTNNLSVLYDNLPGTKNAESVERIKRQ 243

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Db	184	ICSGNSESTOKCGIDVTLCEAFAFRFAVPTKFTPNMLSVLVNLPGTKVNAESVERIKRQ	243
Qy	244	HSOQOTFOLKLMWGNKDDIVKKITODIDLCENSVQRHIGHANLTFEOLRSIMESLP	303
Db	244	HSOQOTFOLKLMWGNKDDIVKKITODIDLCENSVQRHIGHANLTFEOLRSIMESLP	303
Qy	304	GKVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTYQ	363
Db	304	GKVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGIMHALKHSKTYHFPKVTYQ	363
Qy	364	SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKIS	399
Db	364	SLKKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKIS	399

Search completed: September 29, 2004, 13:02:38
Job time : 136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 12:43:33 ; Search time 41 Seconds

(without alignments)
940.800 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 401

Sequence: 1 MNKLCCALVFLDISIKMT.....QKLFLEMIGNQVSVKISCL 401

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.7	69	2 T45354	hypothetical prote
2	7	1.7	102	2 T40795	hypothetical prote
3	7	1.7	119	1 ALHUBR	ig heavy chain V-I
4	7	1.7	139	2 G90414	conserved hypotet
5	7	1.7	165	2 F97290	acetylactate synth
6	7	1.7	170	2 AE1817	hypothetical prote
7	7	1.7	183	2 B84070	hypothetical prote
8	7	1.7	188	2 T26648	hypothetical prote
9	7	1.7	195	2 B89924	conserved hypotet
10	7	1.7	231	2 S74286	hypothetical prote
11	7	1.7	233	2 T50902	Mg protoporhyrin
12	7	1.7	252	2 B69641	cyclase hlsf - Bac
13	7	1.7	252	2 B84097	cyclase hlsf [mpo
14	7	1.7	252	2 A99976	cyclase-like prote
15	7	1.7	258	2 F70307	methionyl aminopep
16	7	1.7	263	2 G82259	probable rare lipop
17	7	1.7	273	2 T50938	DltR protein [mpo
18	7	1.7	283	2 T36121	probable secreted
19	7	1.7	290	2 D81359	probable integral
20	7	1.7	307	2 D85057	hypothetical prote
21	7	1.7	334	2 H75362	hypothetical prote
22	7	1.7	334	2 G86865	hypothetical prote
23	7	1.7	355	2 T01737	hypothetical prote
24	7	1.7	359	2 A11580	endo-1,4-beta-gluc
25	7	1.7	359	2 A11226	endo-1,4-beta-gluc
26	7	1.7	396	2 D82394	GGDEF family prote
27	7	1.7	428	2 A89950	glutamate-1-semial
28	7	1.7	441	2 AG2237	hypothetical prote
29	7	1.7	447	2 A97211	glycosyltransferas

30	7	1.7	497	2 A84956	UDP-N-acetylmutamo
31	7	1.7	504	2 B81437	hypothetical prote
32	7	1.7	501	2 T33404	hypothetical prote
33	7	1.7	518	2 AF0937	hypothetical prote
34	7	1.7	519	2 S33661	rxpr protein - Bac
35	7	1.7	637	2 A54000	sodium/phosphate c
36	7	1.7	637	2 A48189	sodium/phosphate c
37	7	1.7	639	2 B48189	sodium/phosphate c
38	7	1.7	642	2 I46534	renal sodium-depen
39	7	1.7	653	2 A54366	sodium/phosphate c
40	7	1.7	693	2 S49228	sodium-dependent p
41	7	1.7	698	2 H71535	hypothetical prote
42	7	1.7	724	2 T19601	hypothetical prote
43	7	1.7	779	2 AG1978	hypothetical prote
44	7	1.7	805	2 A75014	hypothetical prote
45	7	1.7	808	2 G86208	protein F22G5.28 [

ALIGNMENTS

RESULT 1

T45354
hypothetical protein MLCB57.48 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000

C:Accession: T45354

R:Parkhill, J., Barrell, B.G., Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z16918

A:Accession: T45354

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-69 <PAR>

A:Cross-references: EMBL:Z99494; PIDN:CAB16688.1

A:Experimental source: cosmid B57

C:Genetics:

A:Note: MLCB57.48

Query Match

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 GVVQAGT 135

Db 20 GVVQAGT 26

RESULT 2

T40795
hypothetical protein SPBP87.01c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T40795

R:Beck, A., Reinhardt, R., Lyne, M., Rajandream, M.A., Barrell, B.G.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z21949

A:Accession: T40795

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-102 <BRC>

A:Cross-references: EMBL:AL032684; PIDN:CAA21786.1; GSPDB:GN00067; SPDB:SPBP87.01c

A:Experimental source: strain 972h-; clone pl p887

C:Genetics:

A:Gene: SPDB:SPBP87.01c

A:Map position: 2

A:Insertions: 38/2; 83/3

C:Superfamily: Schizosaccharomyces hypothetical protein SPBP87.01c

Query Match

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 236 SVERIKR 242
Db 2 SVERIKR 8

RESULT 3

AlHUBR

Ig heavy chain V-II region (Bur) - human

C/Species: Homo sapiens (hmn)

C/Date: 22-May-1981 #sequence_revision 22-May-1981 #text_change 02-Sep-1997

C/Accession: A02056

R/Putnam, F.W.; Liu, Y.S.V.; Low, T.L.K.

J. Biol. Chem. 254, 2865-2874, 1979

A/Title: Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal IgA1 protease

A/Reference number: A92249; MUID:79151016; PMID:1071164

A/Contents: myeloma protein Bur

A/Accession: A02056

A/Molecule type: protein

A/Residues: 1-119 <PUT>

A/Note: this is the final paper in a series

C/Genetics: 8

A/Gene: GDB:IGHV@

A/Cross-references: GDB:128528; OMIM:147070

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid

F/15-98/Domain: immunoglobulin homology <IMM>

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/22-96/Disulfide bonds: #status experimental

F/28/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 1.7%; Score 7; DB 1; Length 119;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 129 GVVQAGT 135
Db 10 GVVQAGT 16

|||||
|
|
|
|

RESULT 4

G90414

conserved hypothetical protein [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C/Accession: G90414

R/Shu, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.

arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to Genbank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: G90414

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-139 <KUR>

A/Cross-references: GB:AE006641; NID:g13815734; PIDN:AAK2574.1; GSPDB:GN00155

C/Genetics: 8

A/Gene: SSO2431

Query Match

Best Local Similarity 1.7%; Score 7; DB 2; Length 139;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 323 DQILKIL 329
Db 14 DQILKIL 20

|||||
|
|
|
|

RESULT 5

F97290

acetylactate synthase, small chain [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C/Accession: F97290

R/Molling, U.; Breton, G.; Omelchenko, M.V.; Markova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clof

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: F97290

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-165 <KUR>

A/Cross-references: GB:AE001437; PIDN:AAK8113.1; PID:g15026244; GSPDB:GN00168

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics: 8

A/Gene: CAC3176

C/Superfamily: acetylactate synthase small chain

Query Match

Best Local Similarity 1.7%; Score 7; DB 2; Length 165;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 220 LSVYVDN 226
Db 6 LSVYVDN 12

|||||
|
|
|
|

RESULT 6

AE1817

hypothetical protein all0085 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AE1817

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AE1817

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-170 <KUR>

A/Cross-references: GB:BA000019; PIDN:BAW77609.1; PID:g17135063; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics: 8

A/Gene: all0085

Query Match

Best Local Similarity 1.7%; Score 7; DB 2; Length 170;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 168 VFGLLLT 174
Db 116 VFGLLLT 122

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|
|
|
|

RESULT 7

B84070

hypothetical protein BH3362 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: B84070

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: B84070

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-183 <STO>

A/Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07081.1; GSPDB:GN001

A/Experimental source: strain C-125

C/Genetics:
A:Gene: BH3362

Query Match 1.7%; Score 7; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 299 MESLPGK 305
Db 1 MESLPGK 7

RESULT 8
hypochemical protein Y38A8.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T26648
R:Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans coamid Y38A8.
A:Reference number: Z20251
A:Accession: T26648
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <HML>
A:Cross-references: EMBL:U55855; PIDN:AAA98017.1; GSPDB:GN00020; CESP:Y38A8.1
A:Experimental source: strain Bristol N2; clone Y38A8
C/Genetics:
A:Gene: CESP:Y38A8.1
A:Map position: 2
A:Introns: 143/3

Query Match 1.7%; Score 7; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 232 VNAESVE 238
Db 59 VNAESVE 65

RESULT 9
E89924

conserved hypothetical protein SA1294 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: E89924
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
me, A.; Mutant-i, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <KUR>
A:Cross-references: GB:BA000018; PID:G13701260; PIDN:BA842554.1; GSPDB:GN00149
A:Experimental source: strain N315
C/Genetics:
A:Gene: SA1294
C/Superfamily: Bacillus subtilis hypothetical protein ypjA

Query Match 1.7%; Score 7; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 167 SVFGLL 173
Db 178 SVFGLL 184

RESULT 10
S74286
hypothetical protein YCL012w - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 29-Oct-1999
C/Accession: S74286; S19339
R:Voet, M.; Voelckert, G.
submitted to the Protein Sequence Database, September 1996
A:Reference number: S74277
A:Accession: S74286
A:Molecule type: DNA
A:Residues: 1-231 <VOB>
A:Cross-references: EMBL:X59720; NID:G1907116; PIDN:CAA42347.1; PID:G190713;
R:Oliver, S.G.; Anwar, R.; Brown, A.; Gent, M.E.; Indge, K.J.; James, C.M.; Staveva, L.I
submitted to the Protein Sequence Database, March 1992
A:Reference number: S19337
A:Accession: S19339
A:Molecule type: DNA
A:Residues: 1-121, 'V', 123-142, 'PPLA', 147, 'LTLTL', <OLI>
A:Cross-references: EMBL:X59720; MIPS:YCL012w
A>Note: this sequence has been revised in reference S74286
C/Genetics:
A:Map position: 3L
A>Note: YCL012w

Query Match 1.7%; Score 7; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 135 TPERNTV 141
Db 161 TPERNTV 167

RESULT 11
T50902

Mg protoporphyrin IX monomethyl ester oxidative cyclase subunit [imported] - Rubrivivax
C/Species: Rubrivivax gelatinosus
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2002
C/Accession: T50902
R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynth
A:Reference number: Z25270
A:Accession: T50902
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <NAG>
A:Cross-references: EMBL:AB034704; PIDN:BA84055.1
A:Experimental source: strain IL144
C/Genetics:
A:Gene: bclm
C/Superfamily: magnesium-protoporphyrin O-methyltransferase; b10C homology

Query Match 1.7%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 293 EQLRSLM 299
Db 195 EQLRSLM 201

RESULT 12
B69641

cyclase h1ef - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C/Accession: B69641
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Exlington, J.; Fabret, C.; Ferrar, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsreid, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A;Authors: Lauber, U.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: B69641
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-252 <RUN>
 A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CB15492.1; PID:g2636000
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: hlsF
 C;Superfamily: cyclase hlsF

Query Match 1.7%; Score 7; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LVFLDIS 15
 |||||
 Db 47 LVFLDIS 53

RESULT 13
 B84097
 cyclase hlsF [imported] - *Bacillus halodurans* (strain C-125)
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: B84097
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: B84097
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-252 <STO>
 A;Cross-references: GB:AP00519; GB:BA000004; NID:g10176109; PIDN:BA807297.1; GSPDB:GN0
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: hlsF
 C;Superfamily: cyclase hlsF

Query Match 1.7%; Score 7; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LVFLDIS 15
 |||||
 Db 47 LVFLDIS 53

RESULT 14
 A99976
 cyclase-like protein hlsF [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: A99976
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
 ma, A.; Mizutani-Ui, Y.; Kobayashi, T.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: A99976

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-252 <RUR>
 A;Cross-references: GB:BA000018; PID:g13702631; PIDN:BA843771.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: hlsF
 C;Superfamily: cyclase hlsF

Query Match 1.7%; Score 7; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LVFLDIS 15
 |||||
 Db 47 LVFLDIS 53

RESULT 15
 F70307
 methionyl aminopeptidase - *Aquifex aeolicus*
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 22-Jun-1999
 C;Accession: F70307
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; MUID:98196866; PMID:9537320
 A;Accession: F70307
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-258 <QOF>
 A;Cross-references: GB:AE000672; NID:g2982810; PIDN:AA06448.1; PID:g2982825; GB:AE00065;
 A;Experimental source: strain VFS
 C;Genetics:
 A;Gene: map
 C;Superfamily: *Bacterichia coli* methionyl aminopeptidase

Query Match 1.7%; Score 7; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 302 LPGKRVG 308
 |||||
 Db 146 LPGKRVG 152

Search completed: September 29, 2004, 12:51:18
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 12:35:07 ; Search time 24 Seconds

(without alignments)
870.006 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 401

Sequence: 1 MNKLLCCALVFLDISIKWT.....QKLFLEMIGNVQSVKISCL 401

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 6

Total number of hits satisfying chosen parameters: 594

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	100.0	401	T11B_HUMAN	O00300 homo sapien
2	23	5.7	401	T11B_MOUSE	O08712 mus musculu
3	22	5.5	401	T11B_RAT	O08727 rattus norv
4	1.7	1.7	119	HV3L_HUMAN	P01773 homo sapien
5	1.7	1.7	188	YPA1_CAEEL	Q23236 caenorhabdi
6	1.7	1.7	212	GPH_SYNP7	Q55039 synchococc
7	1.7	1.7	251	HIS6_CHLTR	Q8Kcbo chlorobium
8	1.7	1.7	252	HIS6_BACSD	Q9Kz66 bacillus su
9	1.7	1.7	252	HIS6_BACSD	Q34727 bacillus su
10	1.7	1.7	252	HIS6_STAM	Q99qW8 staphylococ
11	1.7	1.7	252	HIS6_STAM	Q8nu13 staphylococ
12	1.7	1.7	252	HIS6_STAP	Q8Cq92 staphylococ
13	1.7	1.7	258	AMPW_AQUAE	Q66489 aquifex aeo
14	1.7	1.7	263	RLPA_VIBCH	Q9Ctf4 vibrio chol
15	1.7	1.7	328	C170_GIALA	P15799 giardia lam
16	1.7	1.7	401	Y111_SHEON	Q86g03 shewanella
17	1.7	1.7	428	GSA_STAM	Q99c14 staphylococ
18	1.7	1.7	428	GSA_STAM	Q34092 staphylococ
19	1.7	1.7	428	GSA_STAM	Q8nw75 staphylococ
20	1.7	1.7	497	MURF_BUCR1	P57316 buchnera ap
21	1.7	1.7	519	RPRX_BACR1	Q08408 buchnera ap
22	1.7	1.7	602	CYSJ_BUCAP	Q8X9d3 buchnera ap
23	1.7	1.7	637	NPT2_MOUSE	Q06825 mus musculu
24	1.7	1.7	637	NPT2_MOUSE	Q06496 rattus norv
25	1.7	1.7	639	NPT2_HUMAN	Q06495 homo sapien
26	1.7	1.7	639	NPT2_SHEEP	O97704 ovys arien
27	1.7	1.7	642	NPT2_RABYT	Q28620 o renal sod
28	1.7	1.7	650	Y411_HUMAN	Q24295 homo sapien
29	1.7	1.7	738	PSAB_SYNPW	Q9F6t9 synchococc
30	1.7	1.7	742	PSAB_PROMP	Q9F6t9 synchococc
31	1.7	1.7	748	TRBB_EMENI	O47C07 prochloroc
32	1.7	1.7	773	YOD3_CAEEL	P34595 caenorhabdi
33	1.7	1.7	922	B3AT_CHICK	P15575 galinus gall

34	7	1.7	1076	1	CARB_BUCAP	Q8X9d3 buchnera ap
35	7	1.7	1146	1	YHC3_YEAST	P38742 saccharomyc
36	7	1.7	1305	1	CYAF_XENLA	P98999 xenopus lae
37	7	1.7	1515	1	YCF1_YEAST	P29109 saccharomyc
38	7	1.7	1636	1	BUD3_YEAST	P25558 saccharomyc
39	6	1.5	17	1	AU31_LITRA	P82394 litorea ran
40	6	1.5	17	1	AU32_LITRA	P82395 litorea ran
41	6	1.5	17	1	AU33_LITRA	P82396 litorea ran
42	6	1.5	45	1	YA78_ARCFU	O29185 archaeoglob
43	6	1.5	58	1	MT2_CALSI	P55950 callinectes
44	6	1.5	58	1	MT2_CARMA	P55948 carcinus ma
45	6	1.5	66	1	ATPL_STORR	P50017 streptococc

ALIGNMENTS

RESULT 1
T11B_HUMAN STANDARD; PRT: 401 AA.
AC 000300; O60236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy B., Bucay N., Renhan-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., R. R.,
RA Sugis S., Boyle W.D.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heath N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosh S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Beak S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schmechel A., Schein J.E., Jones S.J.M., Marra W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 22-36 AND 378-401.
 RX MEDLINE=98238645; PubMed=95711159.
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
 RA Morinaga T., Tsuda E., Higashio K.,
 RT "Characterization of monomeric and homodimeric forms of
 RT osteoclastogenesis inhibitory factor.";
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
 RN [6]
 RP SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.,
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 RN [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.,
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 RN [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dul E., Appelbaum E.R., Eichman C., DiPietro R., Dods R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.,
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
 RL J. Biol. Chem. 273:14363-14367(1998).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
 RA Morinaga T., Higashio K.,
 RT "Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hofbauer L.C., Neuberger A., Heufelder A.E.,
 RT "Osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC Detected at very low levels in brain, placenta and skeletal

CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -1- INDUCTION: Upregulated by increasing calcium-concentration in the
 CC medium and estrogen. Downregulated by glucocorticoids.
 CC -1- PTM: N-glycosylated. Contains sialic acid residues.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 2 death domains.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@isb-sib.ch).
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 DR EMBL: U94332; AAB53709.1; -.
 DR EMBL: AB002146; BAA25910.1; -.
 DR EMBL: AB008822; BAA32076.1; -.
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: BC030155; AAH30155.1; -.
 DR EMBL: AF134187; AAF20168.1; -.
 DR HSSP: P25942; 1CDF.
 DR Genew: HGNC:11909; TNFRSF11B.
 DR MIM: 602643; -.
 DR GO: GO:0005576; C:extracellular; TAS.
 DR GO: GO:0005125; F:cytokine activity; TAS.
 DR GO: GO:004872; F:receptor activity; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR GO: GO:0001501; P:skeletal development; TAS.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00177; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT SITE 270 365
 FT DISULFID 41 54
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 FT CARBOHYD 98 98
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 3 3
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 FT CONFLICT 263 263
 SO SEQUENCE 401 AA; 46040 MW; EDFA48B67D86C71E CRC64;
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 Best local Similarity 100.0%; Pred. No. 0;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 138 138 R->P (IN STRAINS 129/OLA AND NIH
FT VARIANT 161 161 SWISS).
FT VARIANT 161 161 I->R (IN STRAINS 129/OLA AND NIH
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FT VARIANT 288 288 SWISS).
FT VARIANT 288 288 S->A (IN STRAINS 129/OLA AND NIH
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FT VARIANT 296 296 L->R (IN STRAINS 129/OLA AND NIH
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OY 192 TOKGIDVTLCCEAFRRFAVPTK 214
Db 192 TOKGIDVTLCCEAFRRFAVPTK 214

RESULT 3
ID T11B RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (osteoprotegerin).
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehly R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Upregulated by osteopontin.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U94330; AAB53707.1; -.

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
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DR PROSITE; PSS0652; TNFR_NGFR_270; 270.
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DR PROSITE; PSS0652; TNFR_NGFR_274; 274.
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DR PROSITE; PSS0652; TNFR_NGFR_285; 285.
DR PROSITE; PSS0652; TNFR_NGFR_286; 286.
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DR PROSITE; PSS0652; TNFR_NGFR_289; 289.
DR PROSITE; PSS0652; TNFR_NGFR_290; 290.
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DR PROSITE; PSS0652; TNFR_NGFR_298; 298.
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DR PROSITE; PSS0652; TNFR_NGFR_302; 302.
DR PROSITE; PSS0652; TNFR_NGFR_303; 303.
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DR PROSITE; PSS0652; TNFR_NGFR_305; 305.
DR PROSITE; PSS0652; TNFR_NGFR_306; 306.
DR PROSITE; PSS0652; TNFR_NGFR_307; 307.
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DR PROSITE; PSS0652; TNFR_NGFR_315; 315.
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DR PROSITE; PSS0652; TNFR_NGFR_324; 324.
DR PROSITE; PSS0652; TNFR_NGFR_325; 325.
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DR PROSITE; PSS0652; TNFR_NGFR_334; 334.
DR PROSITE; PSS0652; TNFR_NGFR_335; 335.
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DR PROSITE; PSS0652; TNFR_NGFR_337; 337.
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DR PROSITE; PSS0652; TNFR_NGFR_339; 339.
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DR PROSITE; PSS0652; TNFR_NGFR_341; 341.
DR PROSITE; PSS0652; TNFR_NGFR_342; 342.
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DR PROSITE; PSS0652; TNFR_NGFR_344; 344.
DR PROSITE; PSS0652; TNFR_NGFR_345; 345.
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DR PROSITE; PSS0652; TNFR_NGFR_348; 348.
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DR PROSITE; PSS0652; TNFR_NGFR_356; 356.
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DR PROSITE; PSS0652; TNFR_NGFR_359; 359.
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DR PROSITE; PSS0652; TNFR_NGFR_361; 361.
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DR PROSITE; PSS0652; TNFR_NGFR_363; 363.
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DR PROSITE; PSS0652; TNFR_NGFR_365; 365.
DR PROSITE; PSS0652; TNFR_NGFR_366; 366.
DR PROSITE; PSS0652; TNFR_NGFR_367; 367.
DR PROSITE; PSS0652; TNFR_NGFR_368; 368.
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DR PROSITE; PSS0652; TNFR_NGFR_370; 370.
DR PROSITE; PSS0652; TNFR_NGFR_371; 371.
DR PROSITE; PSS0652; TNFR_NGFR_372; 372.
DR PROSITE; PSS0652; TNFR_NGFR_373; 373.
DR PROSITE; PSS0652; TNFR_NGFR_374; 374.
DR PROSITE; PSS0652; TNFR_NGFR_375; 375.
DR PROSITE; PSS0652; TNFR_NGFR_376; 376.
DR PROSITE; PSS0652; TNFR_NGFR_377; 377.
DR PROSITE; PSS0652; TNFR_NGFR_378; 378.
DR PROSITE; PSS0652; TNFR_NGFR_379; 379.
DR PROSITE; PSS0652; TNFR_NGFR_380; 380.
DR PROSITE; PSS0652; TNFR_NGFR_381; 381.
DR PROSITE; PSS0652; TNFR_NGFR_382; 382.
DR PROSITE; PSS0652; TNFR_NGFR_383; 383.
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DR PROSITE; PSS0652; TNFR_NGFR_386; 386.
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DR PROSITE; PSS0652; TNFR_NGFR_388; 388.
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DR PROSITE; PSS0652; TNFR_NGFR_391; 391.
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DR PROSITE; PSS0652; TNFR_NGFR_393; 393.
DR PROSITE; PSS0652; TNFR_NGFR_394; 394.
DR PROSITE; PSS0652; TNFR_NGFR_395; 395.
DR PROSITE; PSS0652; TNFR_NGFR_396; 396.
DR PROSITE; PSS0652; TNFR_NGFR_397; 397.
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DR PROSITE; PSS0652; TNFR_NGFR_399; 399.
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DR PROSITE; PSS0652; TNFR_NGFR_401; 401.
DR PROSITE; PSS0652; TNFR_NGFR_402; 402.
DR PROSITE; PSS0652; TNFR_NGFR_403; 403.
DR PROSITE; PSS0652; TNFR_NGFR_404; 404.
DR PROSITE; PSS0652; TNFR_NGFR_405; 405.
DR PROSITE; PSS0652; TNFR_NGFR_406; 406.
DR PROSITE; PSS0652; TNFR_NGFR_407; 407.
DR PROSITE; PSS0652; TNFR_NGFR_408; 408.
DR PROSITE; PSS0652; TNFR_NGFR_409; 409.
DR PROSITE; PSS0652; TNFR_NGFR_410; 410.
DR PROSITE; PSS0652; TNFR_NGFR_411; 411.
DR PROSITE; PSS0652; TNFR_NGFR_412; 412.
DR PROSITE; PSS0652; TNFR_NGFR_413; 413.
DR PROSITE; PSS0652; TNFR_NGFR_414; 414.
DR PROSITE; PSS0652; TNFR_NGFR_415; 415.
DR PROSITE; PSS0652; TNFR_NGFR_416; 416.
DR PROSITE; PSS0652; TNFR_NGFR_417; 417.
DR PROSITE; PSS0652; TNFR_NGFR_418; 418.
DR PROSITE; PSS0652; TNFR_NGFR_419; 419.
DR PROSITE; PSS0652; TNFR_NGFR_420; 420.
DR PROSITE; PSS0652; TNFR_NGFR_421; 421.
DR PROSITE; PSS0652; TNFR_NGFR_422; 422.
DR PROSITE; PSS0652; TNFR_NGFR_423; 423.
DR PROSITE; PSS0652; TNFR_NGFR_424; 424.
DR PROSITE; PSS0652; TNFR_NG
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DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT DISULFID 22 96
 FT CARBOHYD 28 28
 FT NON_TER 119 119
 GN N-LINKED (GLCNAC. . .)
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 129 GVWQAGT 135
 Db 10 GVWQAGT 16

RESULT 5

YPAI_CABEL
 ID YPAI_CABEL STANDARD; PRT; 188 AA.
 AC Q23236;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Hypothetical UPF0035 protein Y38A8.1 in chromosome II.
 GN Y38A8.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Hallsworth K.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE NUDIX
 HYDROLASE FAMILY.

-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE UPF0035
 FAMILY.

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 CC -----

CC EMBL; U55855; AAA98017.1; -.
 DR PIR; T26648; T26648.
 DR WormPep; Y38A8.1; CE07570.
 DR InterPro; IPR000086; NUDIX_hydrolase.
 DR InterPro; IPR000059; UPF0035.
 DR Pfam; PF00293; NUDIX; 1.
 DR PRINTS; PR00502; NUDIXFAMILY.
 DR PROSITE; PS00893; NUDIX; 1.
 DR PROSITE; PS01293; UPF0035; 1.
 KW Hypothetical protein; Hydrolase.
 FT DOMAIN 37 58
 FT SEQUENCE 188 AA; 21317 MW; 66CF888F0F12628F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 232 VNABSV 238
 Db 59 VNABSV 65

RESULT 6

GPH_SYN7
 ID GPH_SYN7 STANDARD; PRT; 212 AA.
 AC O56339;
 DT 15-DEC-1998 (Rel. 37; Created)
 DT 15-DEC-1998 (Rel. 37; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Phosphoglycolate phosphatase (EC 3.1.3.18) (PGP).
 GN CBMZ.
 OS Synecchococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
 OX NCBI_Taxid=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96257262; PubMed=8654968;
 RA Liu Y.; Teinoremas N.F.;
 RT "An unusual gene arrangement for the putative chromosome replication
 RT origin and circadian expression of dnaI in Synecchococcus sp. strain
 RT PCC 7942."
 RL Gene 172:105-109(1996).
 CC -1- CATALYTIC ACTIVITY: 2-phosphoglycolate + H(2)O = glycolate +
 CC phosphate.
 CC -1- SIMILARITY: Belongs to the cbbY/cbbZ/gph/yieh family.

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 CC -----

CC EMBL; U33322; AAA75108.1; -.
 DR HAMAP; MF_00495; atypical; 1.
 DR InterPro; IPR005833; Hlgase/hydrlase.
 DR InterPro; IPR005834; Hydrolase.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00413; HADHALOGNASE.
 KW Carbohydrate metabolism; Calvin cycle; Hydrolase.
 SQ SEQUENCE 212 AA; 23572 MW; 8054F39165DECECF CRC64;

Query Match 1.7%; Score 7; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 130 VVQAGTP 136
 Db 126 VVQAGTP 132

RESULT 7

HIS6_CHL7E
 ID HIS6_CHL7E STANDARD; PRT; 251 AA.
 AC Q8KCB0;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hlsf (EC 4.1.3.-) (IGP
 DE synthase cyclase subunit) (IGP synthase subunit hlsf) (IMGP synthase
 DE subunit hlsf) (IGPS subunit hlsf).
 GN HISF OR CTS1514.
 OS Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium.
 OX NCBI_Taxid=1097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49652 / DSM 12025;
 RA Eisen J.A.; Nelson K.E.; Paulsen I.T.; Heidelberg J.F.; Wu M.;
 RA Dodson R.J.; Deboy R.; Gwinn M.L.; Nelson W.C.; Haft D.H.;
 RA Hickey E.K.; Peterson J.D.; Durkin A.S.; Kolonay J.D.; Yang F.;
 RA Holt I.; Umayam L.A.; Mason T.; Brenner M.; Shea T.P.; Parksey D.;
 RA Niemann W.C.; Feldblyum T.V.; Hansen C.L.; Craven M.B.; Radune D.;

RA Vamathavan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tetteijn H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of *Chlorobium tepidum* TLS, a
 RT photoautotrophic, anaerobic, green-sulfur bacterium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
 CC IGP, AICAR and glutamate. The hisF subunit catalyzes the
 CC cyclization activity that produces IGP and AICAR from PRFAR using
 CC the ammonia provided by the hisH subunit (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
 CC carboxamide + L-glutamine = imidazole-glyceral phosphate + 5-
 CC aminomimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the hisA / hisF family.
 CC -----
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 CC -----
 CC EMBL: AE012908; AAM72741.1; -.
 CC TRIGR: CT1514; -.
 DR HAMAP: MF_01013; -; 1.
 DR InterPro: IPR003009; FMN enzyme.
 DR InterPro: IPR006062; His biosynth.
 DR InterPro: IPR004651; HisF.
 DR Pfam: PF00977; His biosynth; 1.
 DR TIGRFAMs: TIGR00735; hisF; 1.
 KW Histidine biosynthesis; Lyase; Complete proteome.
 FT ACT_SITE 11 11 POTENTIAL.
 FT ACT_SITE 130 130 POTENTIAL.
 SQ SEQUENCE 251 AA; 27551 MW; 52A320D7EB04D6E1 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LVFLDIS 15
 Db 47 LVFLDIS 53

RESULT 8
 HIS6_BACSD STANDARD; PRT; 252 AA.
 ID HIS6_BACSD
 AC O9K6Z6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
 DE synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase
 DE subunit hisF) (IGPS subunit hisF).
 GN HISF OR BH3578.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kubara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT halodurans and genomic sequence comparison with *Bacillus subtilis*,"
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to

CC IGP, AICAR and glutamate. The hisF subunit catalyzes the
 CC cyclization activity that produces IGP and AICAR from PRFAR using
 CC the ammonia provided by the hisH subunit (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
 CC carboxamide + L-glutamine = imidazole-glyceral phosphate + 5-
 CC aminomimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the hisA / hisF family.
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 CC -----
 CC EMBL: AP001519; BAB07297.1; -.
 DR PIR: B84097; B84097.
 DR HAMAP: MF_01013; -; 1.
 DR InterPro: IPR003009; FMN enzyme.
 DR InterPro: IPR006062; His biosynth.
 DR InterPro: IPR004651; HisF.
 DR Pfam: PF00977; His biosynth; 1.
 DR TIGRFAMs: TIGR00735; hisF; 1.
 KW Histidine biosynthesis; Lyase; Complete proteome.
 FT ACT_SITE 11 11 POTENTIAL.
 FT ACT_SITE 130 130 POTENTIAL.
 SQ SEQUENCE 252 AA; 27088 MW; ADDE314C48B1E575 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LVFLDIS 15
 Db 47 LVFLDIS 53

RESULT 9
 HIS6_BACSU STANDARD; PRT; 252 AA.
 ID HIS6_BACSU
 AC O34727;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
 DE synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase
 DE subunit hisF) (IGPS subunit hisF).
 GN HISF OR BSU34870.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lazarevic V., Soldo B., Rivolta C., Reynolds S., Maue C.,
 RA Karamata D.;
 RT "Nucleotide sequence of the 300-304 chromosomal segment of *Bacillus*
 RT subtilis,";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capiano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,

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RA Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Guiser M., Fujita Y., Fuma S., Galizly A., Galleron N.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gutserp G., Guy B.J., Haga K., Halech J., Harwood C.R., Hent A.,
RA Hilbert H., Holappell S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Kilaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapilus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Melillo R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Moore D., O'Reilly M., Ogawa K., Ogilawa A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portecelle D., Porwollik S., Prescott A.M.,
RA Presscan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Setiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Socokni A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpeira P., Tognoni A.,
RA Toarso V., Uchiyama S., Vandenbol M., Vannier F., Vaasartoli A.,
RA Viart A., Wambur R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipac A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumestein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hisf subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hisf subunit (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[5-phospho-1-deoxyribulos-1-
CC ylamino)methylidenearino]-1-(5-phosphoribosyl)imidazole-4-
CC carboxamide + L-glutamine = imidazole-glycero-1-phosphate + 5-
CC aminomimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisf and hisf (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the hisa / hisf family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF017113; AAC67299.1; -
DR EMBL: Z99121; CAB15492.1; -
DR PIR: B69641; B69641.
DR Subtilisin_B612600; hisf.
DR HAMAP: MF_01013; -; 1.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR006062; His biosynth.
DR InterPro: IPR004651; Hisf.
DR Pfam: PF00977; His biosynth; 1.
DR TIGRfam: TIGR00735; hisf; 1.
DR Histidine biosynthesis; Lyase; Complete proteome.
FT ACT_SITE 11 11 POTENTIAL.
FT ACT_SITE 130 130 POTENTIAL.
SQ SEQUENCE 252 AA; 27294 MW; B4619A119CB0731A CRC64;
Query Match 1.7%; Score 7; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 9 LVFLDIS 15
Db 47 LVFLDIS 53
RESULT 10
HIS6_STAAH STANDARD; PRT; 252 AA.
ID HIS6_STAAH

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AC 0990W8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisf (bc 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hisf) (ImGP synthase
DE subunit hisf) (IGP subunit hisf).
GN HISF_OR.SAV2673 OR.SA2465.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mitutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Karihisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hisf subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hisf subunit (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[5-phospho-1-deoxyribulos-1-
CC ylamino)methylidenearino]-1-(5-phosphoribosyl)imidazole-4-
CC carboxamide + L-glutamine = imidazole-glycero-1-phosphate + 5-
CC aminomimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hisf and hisf (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the hisa / hisf family.
CC -----
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CC -----
DR EMBL: AP003366; BAB58835.1; -
DR EMBL: AP003138; BAB43771.1; -
DR PIR: A9976; A9976.
DR HAMAP: MF_01013; -; 1.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR006062; His biosynth.
DR InterPro: IPR004651; Hisf.
DR Pfam: PF00977; His biosynth; 1.
DR TIGRfam: TIGR00735; hisf; 1.
DR Histidine biosynthesis; Lyase; Complete proteome.
FT ACT_SITE 11 11 POTENTIAL.
FT ACT_SITE 130 130 POTENTIAL.
SQ SEQUENCE 252 AA; 27529 MW; 963B81CC1C654869 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 9 LVFLDIS 15
Db 47 LVFLDIS 53
RESULT 11
HIS6_STAAH STANDARD; PRT; 252 AA.
ID HIS6_STAAH

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AC Q8NU13;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hlsf (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hlsf) (ImGP synthase
DE subunit hlsf) (IGP subunit hlsf).
GN HISP OR MW2592.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2040717; Pubmed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Agano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hlsf subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hlsf subunit (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
CC aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hlsf and hlsf (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the hlsf / hlsf family.
CC -----
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CC -----
CC EMBL: AP004631; BAB96457.1; -.
CC HAMAP: MF_01013; -.
CC DR InterPro: IPR003009; FMN enzyme.
CC DR InterPro: IPR006062; His biosynth.
CC DR InterPro: IPR004651; Hlsf.
CC DR Pfam: PF00977; His_biosynth; 1.
CC DR TIGRfam: TIGR00735; hlsf; 1.
CC KW Histidine biosynthesis; Lyase; Complete proteome.
CC FT ACT SITE 11 11 POTENTIAL.
CC FT ACT SITE 130 130 POTENTIAL.
CC SQ SEQUENCE 252 AA; 27498 MW; 33F0CAL89198F647 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LVFLDIS 15
DB 47 LVFLDIS 53

RESULT 12
HIS6_STAMP
ID HIS6_STAMP STANDARD; PRT; 252 AA.
AC Q8CQ92;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hlsf (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hlsf) (ImGP synthase
DE subunit hlsf) (IGP subunit hlsf).
GN HISP OR SE0276.

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OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 12228;
RX Pubmed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qiu Z.-Q., Zhao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228)."
RL Mol. Microbiol. 49:1577-1593(2003).
CC -1- FUNCTION: IGP catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hlsf subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hlsf subunit (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
CC aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -1- PATHWAY: Histidine biosynthesis; fifth step.
CC -1- SUBUNIT: Heterodimer of hlsf and hlsf (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the hlsf / hlsf family.
CC -----
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CC -----
CC EMBL: AE016744; AAC03873.1; -.
CC HAMAP: MF_01013; -.
CC DR InterPro: IPR003009; FMN enzyme.
CC DR InterPro: IPR004651; Hlsf.
CC DR InterPro: IPR006062; His biosynth.
CC DR Pfam: PF00977; His_biosynth; 1.
CC DR TIGRfam: TIGR00735; hlsf; 1.
CC KW Histidine biosynthesis; Lyase; Complete proteome.
CC FT ACT SITE 11 11 POTENTIAL.
CC FT ACT SITE 130 130 POTENTIAL.
CC SQ SEQUENCE 252 AA; 27797 MW; 36BD6E3D323AAC9A CRC64;

Query Match 1.7%; Score 7; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LVFLDIS 15
DB 47 LVFLDIS 53

RESULT 13
AMPM_AQUAE
ID AMPM_AQUAE STANDARD; PRT; 258 AA.
AC O66489;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Peptidase M).
GN MAP OR AQ_076.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RX MEDLINE=98196666; Pubmed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjey M., Huber R.,

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RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RL aeolicus.";
CC Nature 397:353-358(1998).
CC -1- FUNCTION: Removes the amino-terminal methionine from nascent
CC proteases (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC preferentially methionine, from peptides and arylamides.
CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M2A.
-----
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-----
DR EMBL/ AE000672; AAC06448.1; -.
DR PIR/ F70307; F70307.
DR HSPSP/ P07906; IC24.
DR MEROS/ M24.001; -.
DR InterPro/ IPR001714; Pept_M24_MAP.
DR InterPro/ IPR002467; Pept_M24_MAP1.
DR InterPro/ IPR000994; Peptidase_M24.
DR Pfam/ PF00557; Peptidase_M24; 1.
DR PRINTS/ PR00599; WAPERTIDNS.
DR TIGRFAMs/ TIGR00500; met_pdae-1; 1.
DR PROSITE/ PS00680; MAP_1; FALSE_NEG.
KW Aminopeptidase; Hydrolase; Cobalt; Complete proteome.
FT METAL 102 102 COBALT 2 (By similarity).
FT METAL 113 113 COBALT 1 AND 2 (By similarity).
FT METAL 176 176 COBALT 1 (By similarity).
FT METAL 211 211 COBALT 1 (By similarity).
FT METAL 242 242 COBALT 1 AND 2 (By similarity).
SQ SEQUENCE 258 AA; 28184 MW; D2EE530C81D09C07 CRC64;

Query March 1.7%; Score 7; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 LPGKKVG 308
Db 146 LPGKKVG 152

RESULT 14
RLPA_VIBCH STANDARD; PRT; 263 AA.
AC Q9KTF4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE RLPA-like lipoprotein precursor.
GN VC0948.
OS Vibrrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_Taxid=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EI TOR N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Debono R.J., Heit D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoti I., Sellers P.,
RA McDonald L., Ueberback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.C., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";

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RL Nature 406:477-483(2000).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: Belongs to the rlpA family.
-----
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-----
DR EMBL/ AE004177; AAP94110.1; -.
DR PIR/ G82259; G82259.
DR TIGR/ VC0948; -.
DR InterPro/ IPR005132; Lipoprotein_13.
DR InterPro/ IPR000437; Prok_lipoprot_s.
DR InterPro/ IPR007730; SPOR.
DR Pfam/ PF03330; Lipoprotein_13; 1.
DR Pfam/ PF05035; SPOR_2.
DR TIGRFAMs/ TIGR00413; rlpA; 2.
DR PROSITE/ PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome; Palmitate.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 263 RLPA-LIKE LIPOPROTEIN.
FT LIPID 17 17 N-palmitoyl cysteine (Potential).
FT LIPID 17 17 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 263 AA; 29290 MW; 3B5B2E7BD67050EB CRC64;

Query March 1.7%; Score 7; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 GVOVAGT 135
Db 155 GVOVAGT 161

RESULT 15
C170_GIALA STANDARD; PRT; 328 AA.
AC C15799;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Surface antigen CRP170 (Fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryote; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_Taxid=5741;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 30957 / WB;
RX MEDLINE=88089405; PubMed=3335828;
RA Adam R.D., Aggarwal A., Lal A.A., de la Cruz V.F., McCutchan T.,
RA Nash T.E.;
RT "Antigenic variation of a cysteine-rich protein in Giardia lamblia.";
RL J. Exp. Med. 167:109-118(1988).
CC -1- MISCELLANEOUS: Cysteine-rich, antigenically variant surface
CC protein.
-----
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-----
DR EMBL/ X06741; CAA29916.1; -.
DR PIR/ A42125; A42125.
DR InterPro/ IPR006212; Furin_repeat.

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DR InterPro; IPR009030; Grow_fac_recep.
KM SMART; SM00261; FU; 3.
Repeat; Antigen.
FT NON_TER 1 1
FT REPEAT 38 102
FT REPEAT 103 167
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 33438 MW; 373A697A30EDCA21 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 CKEGRYL 113
|||
Db 240 CKEGRYL 246

Search completed: September 29, 2004, 12:48:27
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: September 29, 2004, 12:42:18 ; Search time 118 Seconds
(without alignments)
1072.227 Million cell updates/sec

Title: US-09-526-437-2
Perfect score: 401
Sequence: 1 MNKLLCCALVFLDISIKWT.....QKFLFLEMIGNQVQSVKISCL 401

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3197

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacterioph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	8	2.0	64	5 Q9V5P6	Q9V5P6 drosophila
2	8	2.0	109	16 Q81C26	Q81C26 bacillus ce
3	8	2.0	146	13 Q7ZZY4	Q7ZZY4 gallus gall
4	8	2.0	186	13 Q7ZZY5	Q7ZZY5 gallus gall
5	8	2.0	245	4 Q8TB89	Q8TB89 homo sapien
6	8	2.0	269	16 Q87Q28	Q87Q28 vibrio para
7	8	2.0	723	11 Q8C2W6	Q8C2W6 mus musculu
8	8	2.0	759	11 Q9NMS6	Q9NMS6 mus musculu
9	8	2.0	771	11 Q9NMS5	Q9NMS5 mus musculu
10	8	2.0	874	11 Q9JQ97	Q9JQ97 mus musculu
11	8	2.0	1415	4 Q9H7M7	Q9H7M7 homo sapien
12	8	2.0	1510	4 Q8N3D4	Q8N3D4 homo sapien
13	8	2.0	1716	11 Q9NMS7	Q9NMS7 mus musculu
14	8	1.7	65	4 Q43616	Q43616 homo sapien
15	7	1.7	67	5 Q94837	Q94837 giardia lam
16	7	1.7	67	5 Q24963	Q24963 giardia lam

17	7	1.7	69	2 Q33067	Q33067 mycobacteri
18	7	1.7	96	3 Q8J0N1	Q8J0N1 saccharomyc
19	7	1.7	102	3 Q94251	Q94251 schizosacch
20	7	1.7	102	5 Q8SUT4	Q8SUT4 encephalito
21	7	1.7	110	10 Q9LNN6	Q9LNN6 arabidopsis
22	7	1.7	128	10 Q9AVJ3	Q9AVJ3 metaplexis
23	7	1.7	139	17 Q97M16	Q97M16 sulfolobus
24	7	1.7	163	9 Q857L4	Q857L4 mycobacteri
25	7	1.7	165	16 Q97ED7	Q97ED7 clostridium
26	7	1.7	169	11 Q9JKE0	Q9JKE0 ratius norv
27	7	1.7	170	16 Q820K6	Q820K6 anabaena sp
28	7	1.7	180	17 Q8C0L4	Q8C0L4 methanosarc
29	7	1.7	183	16 Q8K7J9	Q8K7J9 bacillus ha
30	7	1.7	190	16 Q92NR6	Q92NR6 rhizobium m
31	7	1.7	191	16 Q98KK7	Q98KK7 rhizobium j
32	7	1.7	195	11 Q9CVT9	Q9CVT9 mus musculu
33	7	1.7	195	16 Q9NUN7	Q9NUN7 staphylococ
34	7	1.7	195	16 Q8NNW7	Q8NNW7 staphylococ
35	7	1.7	202	16 Q8E7A5	Q8E7A5 streptococc
36	7	1.7	202	16 Q8E1U3	Q8E1U3 streptococc
37	7	1.7	204	16 Q9CKB4	Q9CKB4 pasteurella
38	7	1.7	205	12 Q8V5B5	Q8V5B5 pirital vir
39	7	1.7	206	2 Q9REB1	Q9REB1 bartonella
40	7	1.7	209	3 Q874A3	Q874A3 claviopora
41	7	1.7	217	16 Q81Q90	Q81Q90 bacillus an
42	7	1.7	228	2 Q84FS0	Q84FS0 helicobacte
43	7	1.7	228	16 Q88X99	Q88X99 iactobacte
44	7	1.7	233	2 Q9JPA6	Q9JPA6 rhodocycus
45	7	1.7	240	13 Q9DDR8	Q9DDR8 gallus gall

ALIGNMENTS

RESULT 1

ID	Q9V5P6	PRELIMINARY;	PRT;	64 AA.
AC	Q9V5P6	01-MAY-2000 (TRENBLrel. 13, Created)		
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)			
DE	CG7637 protein.			
GN	CG7637.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkley;			
RC	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,			
RA	Butler K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hosetin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jatani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Mlehnina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy U., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Peltan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spieding A.C., Stapleton M., Strong R., Sun E.,
RA Swirskae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Ghibb R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003828; AAF58753.1; -.
DR FlyBase; FBgn0033548; CG7637.
DR InterPro; IPR007264; Nop10P.
DR Pfam; PF04135; Nop10P; 1.
SQ SEQUENCE 64 AA; 7634 MW; B957575B84DEA7CF CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FGLLTQK 176
DB 52 FGLLTQK 59

RESULT 2
QY 081CZ6 PRELIMINARY; PRT; 109 AA.
ID 081CZ6;
AC 081CZ6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phage protein.
DE EC2590.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatala V., Bhattacharya A., Reznik G., Mikhailova N., Lepidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Valunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Feinstein M., Ehrlich S.D.,
RA Overeek R., Kyriades N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017006; AAP09549.1; -.
DR Complete proteome.
SQ SEQUENCE 109 AA; 12642 MW; 1AFEB1C1797AD3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 109;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 FEOLRSIM 299
DB 5 FEOLRSIM 12

RESULT 3
QY 07ZZY4 PRELIMINARY; PRT; 146 AA.
ID 07ZZY4;
AC 07ZZY4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Osteoprotegerin (Fragment).
GN OPG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Bridgman J.T., Johnson A.L.;
RT "Osteoprotegerin (OPG) expression in the hen ovary.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251407; AAP03890.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF_1ike.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
DR NON_TER 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 13; Length 146;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PKRYLHYD 32
DB 25 PKRYLHYD 32

RESULT 4
QY 07ZZY5 PRELIMINARY; PRT; 186 AA.
ID 07ZZY5;
AC 07ZZY5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Decoy receptor 3 (Fragment).
GN DCR3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Bridgman J.T., Johnson A.L.;
RT "DCR3 expression in the hen.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251406; AAP03889.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF_1ike.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
DR Receptor.
DR NON_TER 186
SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACB758E CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 13; Length 186;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 TYVACPD 67

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Db 67 TVCAPCPD 74

RESULT 5

Q8TB89 PRELIMINARY; PRT; 246 AA.

AC Q8TB89; 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DE Similar to tangerin (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

Sequence FROM N.A.

RA Tissue=Muscle;

RA Strauberg R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024207.1; -.

FT NON TER 1

SO SEQUENCE 246 AA; 28083 MW; AAB4E22C4F88124B CRC64;

Query Match 2.0%; Score 8; DB 4; Length 246;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 QLRSLMES 301

Db 110 QLRSLMES 117

RESULT 6

Q87Q28 PRELIMINARY; PRT; 269 AA.

AC Q87Q28; 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DE Putative L1CD1 protein.

GN VPI322.

OS Vibrio parahaemolyticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrrio.

NCBI_TaxID=670;

Sequence FROM N.A.

RA STRAIN=RIWD 221063 / Serotype O3:K6;

RC MEDLINE=22508454; PubMed=12620739;

RA Iijima Y., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Yagunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

RT Lancet 361:743-749(2003).

RL EMBL; AP005077; BAC59585.1; -.

DR InterPro; IPR007074; L1CD.

DR Pfam; PF04991; L1CD; 1.

KW Complete proteome.

SO SEQUENCE 269 AA; 31342 MW; E6180102E9765DB8 CRC64;

Query Match 2.0%; Score 8; DB 16; Length 269;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 LTFEQLRS 297

Db 4 LTFEQLRS 11

RESULT 7

Q8C2W6 PRELIMINARY; PRT; 723 AA.

AC Q8C2W6; 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DE Tangerin (Fragment).

GN KCNK7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

Sequence FROM N.A.

RA MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK087817; BAC40012.1; -.

DR PIR; P70706; P70706.

DR MGI; MGI:1341841; Kcnk7.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

DR SMART; SM00033; CH; 1.

DR PROSITE; PS50021; CH; 1.

FT NON TER 1

SO SEQUENCE 723 AA; 78060 MW; ADF7BA35FDC1E1B8 CRC64;

Query Match 2.0%; Score 8; DB 11; Length 723;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 QLRSLMES 301

Db 587 QLRSLMES 594

RESULT 8

Q99MS6 PRELIMINARY; PRT; 759 AA.

AC Q99MS6; 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DE Tangerin C.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

Sequence FROM N.A.

RA STRAIN=BALB/C;

RA Melichar J.M., Noegel A.A., Korenbaum E.; "Tangerin, a novel Golgi-associated protein with calponin-homology RT domain and CAAX-box.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF305089; AAK32111.1; -.

DR HSSP; Q01082; 1BR.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

DR SMART; SM00033; CH; 1.

DR PROSITE; PS50021; CH; 1.

SO SEQUENCE 759 AA; 83948 MW; 8770323D25E707B4 CRC64;

Query Match 2.0%; Score 8; DB 11; Length 759;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 QLRSLMES 301

Db 623 QLRSLMES 630

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RESULT 9
O99MS5 ID O99MS5 PRELIMINARY; PRT; 771 AA.
AC O99MS5;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Tangerin C'.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Melichar J.M., Noegel A.A., Korenbaum E.;
RT "Tangerin, a novel Golgi-associated protein with calponin-homology
RT domain and CAAX-box.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305090; AAK32112.1; -.
DR HSSP; Q01082; 1BKR.
DR InterPro; IPR001715; Calponin-1like.
DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.
DR PROSITE; PSS0021; CH; 1.
SQ SEQUENCE 771 AA; 85217 MW; 0B3BBE6106C3EAD0 CRC64;

Query Match 2.0%; Score 8; DB 11; Length 771;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 QLRSLMES 301
DB 635 QLRSLMES 642

RESULT 10
O99J97 ID O99J97 PRELIMINARY; PRT; 874 AA.
AC O99J97;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Tangerin B (Similar to KIAA0903 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Melichar J.M., Noegel A.A., Korenbaum E.;
RT "Tangerin, a novel Golgi-associated protein with calponin-homology
RT domain and CAAX-box.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305088; AAK32110.1; -.
DR EMBL; BC004660; AAK04660.1; -.
DR HSSP; Q01082; 1BKR.
DR InterPro; IPR001715; Calponin-1like.
DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.
DR PROSITE; PSS0021; CH; 1.
SQ SEQUENCE 874 AA; 95560 MW; 94803958BCD5BBD CRC64;

Query Match 2.0%; Score 8; DB 11; Length 874;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 294 QLRSLMES 301
DB 738 QLRSLMES 745

RESULT 11
O9H7M7 ID O9H7M7 PRELIMINARY; PRT; 1415 AA.
AC O9H7M7;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE FLJ00043 protein (Fragment).
GN FLJ00043.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024451; BAB15741.1; -.
DR HSSP; Q01082; 1BKR.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR InterPro; IPR001715; Calponin-1like.
DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER; 1.
DR PROSITE; PSS0021; CH; 1.
FT NON TER 1
SQ SEQUENCE 1415 AA; 148907 MW; 5C49474E2555940E CRC64;

Query Match 2.0%; Score 8; DB 4; Length 1415;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 QLRSLMES 301
DB 1279 QLRSLMES 1286

RESULT 12
O8N3D4 ID O8N3D4 PRELIMINARY; PRT; 1510 AA.
AC O8N3D4;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP762C186.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834433; CAD39093.1; -.
DR InterPro; IPR001715; Calponin-1like.
DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.
DR PROSITE; PSS0021; CH; 1.
KM Hypothetical protein.

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FT NON TER 1 1
SQ SEQUENCE 1510 AA; 160311 MW; 15C2B93E44528E39 CRC64;

Query Match
Best Local Similarity 2.0%; Score 8; DB 4; Length 1510;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 294 QLRSLMES 301
Db 1374 QLRSLMES 1381

RESULT 13

ID 099MS7 PRELIMINARY; PRT: 1716 AA.

AC 099MS7; DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tanagerin A.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCB1_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;
RA Melichar J.M., Noegel A.A., Korenbaum E.;

RT "Tangerin, a novel Golgi-associated protein with calponin-homology
RT domain and CAX-box."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF305087; AAK32109.1; -.

DR HSP; 001082; 18KR.
DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.
DR SMART; SM00033; CH; 1.

DR PROSITE; PS50021; CH; 1.
SQ SEQUENCE 1716 AA; 164834 MW; CE9587BAAD06CA00 CRC64;

OY 294 QLRSLMES 301
Db 1580 QLRSLMES 1587

RESULT 14

ID 043616 PRELIMINARY; PRT: 65 AA.

AC 043616; DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Malignancy-associated protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Hepatoma;
RA Ljubimova J.Y., Demetriadou A.A.;

RT "A novel gene associated with liver cirrhosis and neoplasia, U.S.
RT Patent, pending."

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF041410; AAB99789.1; -.
FT NON TER 1
SQ SEQUENCE 65 AA; 7483 MW; 9D1F620D1FDAEE48 CRC64;

Query Match
Best Local Similarity 1.7%; Score 7; DB 4; Length 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 SCPGFG 129
Db 12 SCPGFG 18

RESULT 15

ID 094837 PRELIMINARY; PRT: 67 AA.

AC 094837; DT 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Variant-specific surface protein (Fragment).

OS Giardia lamblia (Giardia intestinalis).

OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.

OX NCB1_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=WB46;
RX MEDLINE=94301794; PubMed=8029018;

RA Yang Y., Adam R.D.;

RT "Allele-specific expression of a variant-specific surface protein
RT (VSP) of Giardia lamblia."

RL Nucleic Acids Res. 22:2102-2108 (1994).

DR EMBL; U25060; AAA57226.1; -.

FT NON TER 1
SQ SEQUENCE 67 AA; 7055 MW; AC38B713167FE339 CRC64;

OY 107 CKGRYL 113
Db 23 CKGRYL 29

Query Match
Best Local Similarity 1.7%; Score 7; DB 5; Length 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: September 29, 2004, 12:50:32
Job time : 121 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model1

Run on: September 29, 2004, 12:45:53 ; Search time 32 Seconds
(without alignments)
646.938 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 401
Sequence: 1 MNKLCCALVFLDISIKMTT.....QKFLFMIGNQGVSKISCL 401

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 6

Total number of hits satisfying chosen parameters: 831

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	100.0	401	3	US-09-153-927-1
2	401	100.0	401	4	US-09-072-993C-1
3	401	100.0	401	4	US-10-039-785-5
4	300	74.8	401	3	US-08-974-022-6
5	300	74.8	401	3	US-09-042-785A-12
6	300	74.8	401	3	US-08-795-445A-6
7	300	74.8	401	3	US-08-795-447A-6
8	300	74.8	401	3	US-08-974-186-6
9	300	74.8	401	3	US-08-795-446B-6
10	300	74.8	401	4	US-08-706-945D-128
11	300	74.8	401	4	US-08-577-788C-6
12	300	74.8	401	4	US-08-577-788C-56
13	161	40.1	401	4	US-09-632-277A-3
14	147	36.7	147	4	US-09-527-236A-20
15	147	36.7	147	4	US-09-756-854-20
16	146	36.4	146	4	US-09-523-323-58
17	144	35.9	364	4	US-08-706-945D-142
18	139	34.7	139	4	US-08-706-945D-130
19	23	5.7	364	4	US-08-706-945D-141
20	23	5.7	401	3	US-08-974-022-4
21	23	5.7	401	3	US-09-042-785A-13
22	23	5.7	401	3	US-08-795-445A-4
23	23	5.7	401	3	US-08-795-447A-4
24	23	5.7	401	3	US-08-974-186-4
25	23	5.7	401	3	US-08-795-446B-4
26	23	5.7	401	4	US-08-706-945D-126
27	23	5.7	401	4	US-08-577-788C-4

28	23	5.7	401	4	US-08-577-788C-54	Sequence 54, Appl
29	22	5.5	401	3	US-08-974-022-2	Sequence 2, Appl
30	22	5.5	401	3	US-08-795-445A-2	Sequence 2, Appl
31	22	5.5	401	3	US-08-795-447A-2	Sequence 2, Appl
32	22	5.5	401	3	US-08-974-186-2	Sequence 2, Appl
33	22	5.5	401	3	US-08-795-446B-2	Sequence 2, Appl
34	22	5.5	401	4	US-08-706-945D-124	Sequence 124, App
35	22	5.5	401	4	US-08-577-788C-2	Sequence 2, Appl
36	22	5.5	401	4	US-08-577-788C-55	Sequence 55, Appl
37	20	5.0	174	4	US-08-706-945D-136	Sequence 136, App
38	20	5.0	208	4	US-08-577-788C-50	Sequence 50, Appl
39	18	4.5	19	3	US-08-974-022-40	Sequence 40, Appl
40	18	4.5	19	3	US-08-795-445A-40	Sequence 40, Appl
41	18	4.5	19	3	US-08-795-447A-40	Sequence 40, Appl
42	18	4.5	19	3	US-08-974-186-40	Sequence 40, Appl
43	18	4.5	19	3	US-08-795-446B-40	Sequence 40, Appl
44	18	4.5	19	4	US-08-706-945D-62	Sequence 62, Appl
45	18	4.5	19	4	US-08-577-788C-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1									
US-09-153-927-1									
Sequence 1, Application US/09153927A									
Patent No. 6297022									
GENERAL INFORMATION:									
APPLICANT: McDonnell, Peter C.									
APPLICANT: Young, Peter R.									
TITLE OF INVENTION: A Method of Identifying Agonists and									
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3									
FILE REFERENCE: GHS0031									
CURRENT APPLICATION NUMBER: US/09/153,927A									
CURRENT FILING DATE: 1998-09-16									
EARLIER APPLICATION NUMBER: 60/061,334									
EARLIER FILING DATE: 1997-10-08									
NUMBER OF SEQ ID NOS: 11									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 1									
LENGTH: 401									
TYPE: PRT									
ORGANISM: Human									
US-09-153-927-1									
Query Match									
Best Local Similarity 100.0%; Score 401; DB 3; Length 401;									
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	121	HRSCPFGVVOAGTTPRNVTCKRCPPGFPNSNETSSAKPCKHTNCSVFGLLLTQKNAT	180						
Db	121	HRSCPFGVVOAGTTPRNVTCKRCPPGFPNSNETSSAKPCKHTNCSVFGLLLTQKNAT	180						
Qy	181	HDNCSGNSSTQKCGIDVTLCEBAPFRFAVPTKFTPNMLSVLYDNLPGTKVNAESVERI	240						
Db	181	HDNCSGNSSTQKCGIDVTLCEBAPFRFAVPTKFTPNMLSVLYDNLPGTKVNAESVERI	240						
Qy	241	KRQSSSQETFPOLLKMKQKQODIYKTIIDIDLCNSVQKHGIANLTFEQLRLME	300						
Db	241	KRQSSSQETFPOLLKMKQKQODIYKTIIDIDLCNSVQKHGIANLTFEQLRLME	300						
Qy	301	SLPKKVGADIEKTIKACKPSDQILKLSLMIKNGDDTLKGLMALKHSKTYHPKPT	360						
Db	301	SLPKKVGADIEKTIKACKPSDQILKLSLMIKNGDDTLKGLMALKHSKTYHPKPT	360						

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Db      301 SLPGKVGADIEKTIACKPSDQILKLSLWIRKNGDDPTLKGMLHAKSHYHPKT 360
Qy      361 VTOSLKTIRFLHSFTMYKLYOKLFLEMIGNOVSVISCL 401
Db      361 VTOSLKTIRFLHSFTMYKLYOKLFLEMIGNOVSVISCL 401

RESULT 2
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1

Query Match      100.0%; Score 401; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNTRNHRVCEKGRYLEIEFCLK 120
Db      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNTRNHRVCEKGRYLEIEFCLK 120
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Qy      121 HRSCEPFGVVOAGTPEPRNTVCKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
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Db      181 HDNICSNSESTOKCGIDVTLCBEAFPRFAVPTKFTPMNLSTLVNDLPGTKVAESVERI 240
Qy      241 KROHSSQEQTFOLKLMKHQNKDDIVKTIIDIDLCENSVORHIGHANLTFFQLRLSME 300
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Qy      241 KROHSSQEQTFOLKLMKHQNKDDIVKTIIDIDLCENSVORHIGHANLTFFQLRLSME 300
Db      241 KROHSSQEQTFOLKLMKHQNKDDIVKTIIDIDLCENSVORHIGHANLTFFQLRLSME 300
Qy      301 SLPGKVGADIEKTIACKPSDQILKLSLWIRKNGDDPTLKGMLHAKSHYHPKT 360
Db      301 SLPGKVGADIEKTIACKPSDQILKLSLWIRKNGDDPTLKGMLHAKSHYHPKT 360
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Db      361 VTOSLKTIRFLHSFTMYKLYOKLFLEMIGNOVSVISCL 401

RESULT 3
US-10-039-785-5
; Sequence 5, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
```

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; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-5

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MNKLCCALVFLDISIKMTTOETPPPKYLYHYDEBESHQLLCDKCPGTYLKQHTAKMKT 60
Db      1 MNKLCCALVFLDISIKMTTOETPPPKYLYHYDEBESHQLLCDKCPGTYLKQHTAKMKT 60
Qy      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNTRNHRVCEKGRYLEIEFCLK 120
Db      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVKQECNTRNHRVCEKGRYLEIEFCLK 120
Qy      121 HRSCEPFGVVOAGTPEPRNTVCKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
Db      121 HRSCEPFGVVOAGTPEPRNTVCKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
Qy      121 HRSCEPFGVVOAGTPEPRNTVCKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
Db      121 HRSCEPFGVVOAGTPEPRNTVCKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
Qy      181 HDNICSNSESTOKCGIDVTLCBEAFPRFAVPTKFTPMNLSTLVNDLPGTKVAESVERI 240
Db      181 HDNICSNSESTOKCGIDVTLCBEAFPRFAVPTKFTPMNLSTLVNDLPGTKVAESVERI 240
Qy      241 KROHSSQEQTFOLKLMKHQNKDDIVKTIIDIDLCENSVORHIGHANLTFFQLRLSME 300
Db      241 KROHSSQEQTFOLKLMKHQNKDDIVKTIIDIDLCENSVORHIGHANLTFFQLRLSME 300
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Qy      301 SLPGKVGADIEKTIACKPSDQILKLSLWIRKNGDDPTLKGMLHAKSHYHPKT 360
Db      301 SLPGKVGADIEKTIACKPSDQILKLSLWIRKNGDDPTLKGMLHAKSHYHPKT 360
Qy      361 VTOSLKTIRFLHSFTMYKLYOKLFLEMIGNOVSVISCL 401
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RESULT 4
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
```

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-6

Query Match 74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9.4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNKLICALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHTAKKKT 60
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DB 61 VCACPDPHYTDSWHTSDECLYCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPGGVQAGTPERNTVCKRCPDGFSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVQAGTPERNTVCKRCPDGFSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTKVNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTKVNAESVERI 240
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DB 241 KROHSSOEQTQLKLMKHQNKQDIIKKIIOIDILCENSVOIRHIGHANLTFEOLRSIME 300
QY 301 SLPGKVAEADIETIKACKPSDOIILKLSMRINKGODDTLKGIMHALKHSKTYHPKPT 360
DB 301 SLPGKVAEADIETIKACKPSDOIILKLSMRINKGODDTLKGIMHALKHSKTYHPKPT 360
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DB 361 VTOSLAKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 5
US-09-042-785A-12
Sequence 12, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Buefield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
AND USES THEREFOR
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-12

Query Match 74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9.4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLICALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHTAKKKT 60
DB 1 MNKLICALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHTAKKKT 60
QY 61 VCACPDPHYTDSWHTSDECLYCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLK 120
DB 61 VCACPDPHYTDSWHTSDECLYCSPVCKELQYVQECNRTHNRVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPGGVQAGTPERNTVCKRCPDGFSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVQAGTPERNTVCKRCPDGFSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTKVNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTKVNAESVERI 240
QY 241 KROHSSOEQTQLKLMKHQNKQDIIKKIIOIDILCENSVOIRHIGHANLTFEOLRSIME 300
DB 241 KROHSSOEQTQLKLMKHQNKQDIIKKIIOIDILCENSVOIRHIGHANLTFEOLRSIME 300
QY 301 SLPGKVAEADIETIKACKPSDOIILKLSMRINKGODDTLKGIMHALKHSKTYHPKPT 360
DB 301 SLPGKVAEADIETIKACKPSDOIILKLSMRINKGODDTLKGIMHALKHSKTYHPKPT 360
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DB 361 VTOSLAKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 6
US-08-795-445A-6
Sequence 6, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.

```

? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: 1840 Denavilland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/795,445A
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-795-445A-6

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Query Match          74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9.4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQHTAKMT 60
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DB 61 VCAPCPDHYTDSWHTSDDECLYCSPVCKELQYVQECNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRCSPGFGVQAGTPERNIVCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
DB 121 HRCSPGFGVQAGTPERNIVCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
QY 181 HDNICGNSSESTQKCGIDVTLCEAFPRFPAVPTKFTPNMLSVLYVDNLPGTKVAESVERI 240
DB 181 HDNICGNSSESTQKCGIDVTLCEAFPRFPAVPTKFTPNMLSVLYVDNLPGTKVAESVERI 240
QY 241 KRQSSQEQTFQQLKLMKQNKQDIYKKIIOIDILCENSVOHRIGHANLTFEQLSLME 300
DB 241 KRQSSQEQTFQQLKLMKQNKQDIYKKIIOIDILCENSVOHRIGHANLTFEQLSLME 300
QY 301 SLPGKVGABEDIKTIKACRPSDQILKLSIMRIKNGDDTLKGLMHALKHSKTYHPKPT 360
DB 301 SLPGKVGABEDIKTIKACRPSDQILKLSIMRIKNGDDTLKGLMHALKHSKTYHPKPT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

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```

RESULT 7
US-08-795-447A-6
; Sequence 6, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Lacey, David L.

```

```

? APPLICANT: Boyle, William J.
? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: Osteoprotegerin
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: One Amgen Center Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91362-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/795,447A
? FILING DATE:
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378D2
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-795-447A-6

```

```

Query Match          74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9.4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQHTAKMT 60
DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQHTAKMT 60
QY 61 VCAPCPDHYTDSWHTSDDECLYCSPVCKELQYVQECNRTNHNVCCKEGRYLEIEFCLK 120
DB 61 VCAPCPDHYTDSWHTSDDECLYCSPVCKELQYVQECNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRCSPGFGVQAGTPERNIVCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
DB 121 HRCSPGFGVQAGTPERNIVCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNAT 180
QY 181 HDNICGNSSESTQKCGIDVTLCEAFPRFPAVPTKFTPNMLSVLYVDNLPGTKVAESVERI 240
DB 181 HDNICGNSSESTQKCGIDVTLCEAFPRFPAVPTKFTPNMLSVLYVDNLPGTKVAESVERI 240
QY 241 KRQSSQEQTFQQLKLMKQNKQDIYKKIIOIDILCENSVOHRIGHANLTFEQLSLME 300
DB 241 KRQSSQEQTFQQLKLMKQNKQDIYKKIIOIDILCENSVOHRIGHANLTFEQLSLME 300
QY 301 SLPGKVGABEDIKTIKACRPSDQILKLSIMRIKNGDDTLKGLMHALKHSKTYHPKPT 360
DB 301 SLPGKVGABEDIKTIKACRPSDQILKLSIMRIKNGDDTLKGLMHALKHSKTYHPKPT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

```

```

RESULT 8
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.

```

APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-6

Query Match 74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9,4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLCCALVFLDISIKWTTQETPPPKYLHYDEBESHQLLCDKCPPTGYLKHCHTAKWKT 60
DB 1 MNKLCCALVFLDISIKWTTQETPPPKYLHYDEBESHQLLCDKCPPTGYLKHCHTAKWKT 60
QY 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNRCVCECKEGRYLEIEFCLK 120
DB 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNRCVCECKEGRYLEIEFCLK 120
QY 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLVDNLPGTVMASVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLVDNLPGTVMASVERI 240
QY 241 KROHSSQEQTFQLLKLMKQKADIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
DB 241 KROHSSQEQTFQLLKLMKQKADIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
QY 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRINKGQDPTLKGMLAKSKSTYHFPKT 360
DB 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRINKGQDPTLKGMLAKSKSTYHFPKT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIQNOVSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIQNOVSVKISCL 401

RESULT 9
US-08-795-446B-6
Sequence 6, Application US/08795446B
Patent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1640 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-6

Query Match 74.8%; Score 300; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 9,4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLCCALVFLDISIKWTTQETPPPKYLHYDEBESHQLLCDKCPPTGYLKHCHTAKWKT 60
DB 1 MNKLCCALVFLDISIKWTTQETPPPKYLHYDEBESHQLLCDKCPPTGYLKHCHTAKWKT 60
QY 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNRCVCECKEGRYLEIEFCLK 120
DB 61 VCAPCPDHYTDSMTSDECLYCSPVCKELQYVQECNRTNRCVCECKEGRYLEIEFCLK 120
QY 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCPGRGVVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLVDNLPGTVMASVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLVDNLPGTVMASVERI 240
QY 241 KROHSSQEQTFQLLKLMKQKADIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
DB 241 KROHSSQEQTFQLLKLMKQKADIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
QY 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRINKGQDPTLKGMLAKSKSTYHFPKT 360
DB 301 SLPGKVGAEDEIKTIKACRPSDQILKLSLWRINKGQDPTLKGMLAKSKSTYHFPKT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIQNOVSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIQNOVSVKISCL 401

RESULT 10
US-08-706-945D-128
Sequence 128, Application US/08706945D
Patent No. 6169027
GENERAL INFORMATION:

```

; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIORITY FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-706-945D-128

```

```

Query Match          74.8%; Score 300; DB 4; Length 401;
Best Local Similarity 99.8%; Pred. No. 9,4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Db      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Qy      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Db      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Qy      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Db      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Qy      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
Db      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
Qy      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
Db      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
Qy      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
Db      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
Qy      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

```

```

RESULT 11
US-08-577-788C-6
; Sequence 6, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-577-788C-6

```

```

Query Match          74.8%; Score 300; DB 4; Length 401;

```

```

Best Local Similarity 99.8%; Pred. No. 9,4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Db      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Qy      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Db      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Qy      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Db      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Qy      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
Db      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
Qy      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
Db      241 KROHSSQEQTFOLLKLMKQNKQKADIVKIIODIDLCENSVORHIGHANLTFEQLSLME 300
Qy      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
Db      301 SLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGMLHALKHSKTYHFPKT 360
Qy      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db      361 VTQSLKKTIRPLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

```

```

RESULT 12
US-08-577-788C-56
; Sequence 56, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-577-788C-56

```

```

Query Match          74.8%; Score 300; DB 4; Length 401;
Best Local Similarity 99.8%; Pred. No. 9,4e-288;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Db      1 MNKLCCALVPLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCTAKMKT 60
Qy      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Db      61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNTHNRVCEKGRYLEIEFCLK 120
Qy      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Db      121 HRSCPPGFGVVOAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGLLITQKGNAT 180
Qy      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240
Db      181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNDLPGTKVAASVERI 240

```

Qy 241 KROHSEOTFOLKLMWGNKDDIVKKIIOIDILCENSVOHGHANLTFEOLRSIME 300
 Db 241 KROHSEOTFOLKLMWGNKDDIVKKIIOIDILCENSVOHGHANLTFEOLRSIME 300
 Qy 301 SLPGKVGAEIETIKAKCPSPDQILKLSLWIRINGDQDTLKGMLAKSKTYHPKT 360
 Db 301 SLPGKVGAEIETIKAKCPSPDQILKLSLWIRINGDQDTLKGMLAKSKTYHPKT 360
 Qy 361 VTQSLKTIKIRFLHSFTWYKLYOKLFLEMIGNOVOSVKISCL 401
 Db 361 VTQSLKTIKIRFLHSFTWYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 13
 US-09-632-277A-3
 ; Sequence 3, Application US/09632277A
 ; Patent No. 659716
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsu, Hailing
 ; TITLE OF INVENTION: TNF3 A No. 659716el Member of the TNF-Receptor Supergene Family
 ; FILE REFERENCE: 01017/35549A
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US/09/632,277A
 ; PRIOR FILING DATE: 1999-08-04
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 161
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: Mus musculus ORG
 US-09-632-277A-3

Query Match 40.1%; Score 161; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 6e-151;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 26 PKYLAHYDEETSHQLCDKCPGGTYLKQCHTAKMKTVCAPCPDHYYTDSMTSDCLYCSP 85
 Db 1 PKYLAHYDEETSHQLCDKCPGGTYLKQCHTAKMKTVCAPCPDHYYTDSMTSDCLYCSP 60
 Qy 86 VCKELQYVKECNCNTHNVCECKGRVYIEFCLKHSRCPGFGVQAGTERNTVCRC 145
 Db 61 VCKELQYVKECNCNTHNVCECKGRVYIEFCLKHSRCPGFGVQAGTERNTVCRC 120
 Qy 146 PDGFFSNETSAPCRKHTNCSVFGLLTQKGNATHDNICS 186
 Db 121 PDGFFSNETSAPCRKHTNCSVFGLLTQKGNATHDNICS 161

RESULT 14
 US-09-527-236A-20
 ; Sequence 20, Application US/09527236A
 ; Patent No. 6358508
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner L.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; FILE REFERENCE: PF375F1
 ; CURRENT APPLICATION NUMBER: US/09/527,236A
 ; CURRENT FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/052,991
 ; PRIOR FILING DATE: 1997-06-11
 ; PRIOR APPLICATION NUMBER: 09/095,094
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/126,019
 ; PRIOR FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: 60/134,220
 ; PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 147
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-527-236A-20

Query Match 36.7%; Score 147; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 3.6e-137;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 40 LCDKCPGGTYLKQCHTAKMKTVCAPCPDHYYTDSMTSDCLYCSPVCKELQYVKECNCN 99
 Db 1 LCDKCPGGTYLKQCHTAKMKTVCAPCPDHYYTDSMTSDCLYCSPVCKELQYVKECNCN 60
 Qy 100 THNRVCECKGRVYIEFCLKHSRCPGFGVQAGTERNTVCRCPDGFFSNETSAP 159
 Db 61 THNRVCECKGRVYIEFCLKHSRCPGFGVQAGTERNTVCRCPDGFFSNETSAP 120
 Qy 160 CRKHTNCSVFGLLTQKGNATHDNICS 186
 Db 121 CRKHTNCSVFGLLTQKGNATHDNICS 147

RESULT 15
 US-09-756-854-20
 ; Sequence 20, Application US/09756854
 ; Patent No. 6667390
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/756,854
 ; FILING DATE: 10-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/095,094
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoover, Kenley K.
 ; REGISTRATION NUMBER: 40,302
 ; REFERENCE/DOCKET NUMBER: PF375
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 147 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-09-756-854-20
 Query Match 36.7%; Score 147; DB 4; Length 147;

Best Local Similarity 100.0%; Pred. No. 3.6e-137;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	40	LCDKCPGTYLKQHCIAKMKTVCAPCPDHYTDSWHTSDECLYCSPYCKELQYVKQECNR	99
Db	1	LCDKCPGTYLKQHCIAKMKTVCAPCPDHYTDSWHTSDECLYCSPYCKELQYVKQECNR	60
QY	100	THNRVCECKEGRYIEIEFCLKHSRCPGPGVQAQTPERNVCKRCPDGFFSNETS	159
Db	61	THNRVCECKEGRYIEIEFCLKHSRCPGPGVQAQTPERNVCKRCPDGFFSNETS	120
QY	160	CRKHTNCSVFGLLLTQKGNATHDNICS	186
Db	121	CRKHTNCSVFGLLLTQKGNATHDNICS	147

Search completed: September 29, 2004, 12:51:54
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 29, 2004, 12:23:11; Search time 33 Seconds
(without alignments)
627.334 Million cell updates/sec

Title: US-09-526-437-2
Perfect score: 2200
Sequence: 1 MNKLCCALVFLDISIKMTT.....QKLFLEMIGNQVSVKISCL 401

Scoring table: BLOSUM62
Gapop: 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2200	100.0	401	3	US-09-153-927-1
2	2200	100.0	401	4	US-09-072-993C-1
3	2200	100.0	401	4	US-10-039-785-5
4	2192	99.6	401	3	US-08-974-022-6
5	2192	99.6	401	3	US-09-042-785A-12
6	2192	99.6	401	3	US-08-795-445A-6
7	2192	99.6	401	3	US-08-795-447A-6
8	2192	99.6	401	3	US-08-974-186-6
9	2192	99.6	401	3	US-08-795-446B-6
10	2192	99.6	401	4	US-08-706-945D-128
11	2192	99.6	401	4	US-08-577-788C-6
12	2192	99.6	401	4	US-08-577-788C-56
13	2192	99.6	401	4	US-08-706-945D-142
14	2192	99.6	401	3	US-08-974-022-2
15	2192	99.6	401	3	US-08-795-445A-2
16	2192	99.6	401	3	US-08-795-447A-2
17	2192	99.6	401	3	US-08-974-186-2
18	2192	99.6	401	3	US-08-795-446B-2
19	2192	99.6	401	4	US-08-706-945D-124
20	2192	99.6	401	4	US-08-577-788C-2
21	2192	99.6	401	4	US-08-577-788C-55
22	2192	99.6	401	3	US-08-974-022-4
23	2192	99.6	401	3	US-09-042-785A-13
24	2192	99.6	401	3	US-08-795-445A-4
25	2192	99.6	401	3	US-08-795-447A-4
26	2192	99.6	401	3	US-08-974-186-4
27	2192	99.6	401	3	US-08-795-446B-4

28	1900	86.4	401	4	US-08-706-945D-126	Sequence 126, App
29	1900	86.4	401	4	US-08-577-788C-4	Sequence 4, Appli
30	1900	86.4	401	4	US-08-577-788C-54	Sequence 54, Appli
31	1728	78.5	364	4	US-08-706-945D-141	Sequence 141, App
32	1030	46.8	208	4	US-08-577-788C-50	Sequence 50, Appli
33	945	43.0	161	4	US-09-632-277A-3	Sequence 3, Appli
34	865	39.3	147	4	US-09-527-236A-20	Sequence 20, Appli
35	865	39.3	147	4	US-09-527-236A-20	Sequence 20, Appli
36	861	39.1	146	4	US-09-523-323-58	Sequence 58, Appli
37	859	39.0	174	4	US-08-706-945D-136	Sequence 136, App
38	827	37.6	139	4	US-08-706-945D-130	Sequence 130, App
39	444	20.2	300	2	US-08-794-796-2	Sequence 2, Appli
40	444	20.2	300	4	US-09-632-277A-2	Sequence 2, Appli
41	444	20.2	300	4	US-09-523-323-52	Sequence 52, Appli
42	435.5	19.8	211	3	US-09-286-529-20	Sequence 20, Appli
43	435.5	19.8	299	3	US-09-286-529-17	Sequence 17, Appli
44	406	18.5	146	4	US-09-523-323-59	Sequence 59, Appli
45	344	15.6	258	4	US-09-579-845-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1					
US-09-153-927-1					
Sequence 1, Application US/09153927A					
Patent No. 6297022					
GENERAL INFORMATION:					
APPLICANT: McDonnell, Peter C.					
APPLICANT: Young, Peter R.					
APPLICANT: Zou, Jun					
TITLE OF INVENTION: A Method of Identifying Agonists and					
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3					
FILE OF INVENTION: AND TR5					
FILE REFERENCE: GH50031					
CURRENT APPLICATION NUMBER: US/09/153.927A					
CURRENT FILING DATE: 1998-09-16					
EARLIER APPLICATION NUMBER: 60/061.334					
EARLIER FILING DATE: 1997-10-08					
NUMBER OF SEQ ID NOS: 11					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 1					
LENGTH: 401					
TYPE: PRT					
ORGANISM: Human					
US-09-153-927-1					
Query Match					
Best Local Similarity 100.0%; Pred. No. 3.2e-193; Length 401;					
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MNKLCCALVFLDISIKMTTGETPPKYLHYDEBTSQQLCDKCPPTLYLKHQCTAKMT	60		
DB	1	MNKLCCALVFLDISIKMTTGETPPKYLHYDEBTSQQLCDKCPPTLYLKHQCTAKMT	60		
QY	61	VCACPDHYTDSWHTSDECIYCSVPCKELOYVQECRTNRRCECKEGYLIBEFLK	120		
DB	61	VCACPDHYTDSWHTSDECIYCSVPCKELOYVQECRTNRRCECKEGYLIBEFLK	120		
QY	121	HRSPGPGVVOAGTPERNVCKRCPOGPFSENSSAPCRKHNCVSFGLLLTOKGNAT	180		
DB	121	HRSPGPGVVOAGTPERNVCKRCPOGPFSENSSAPCRKHNCVSFGLLLTOKGNAT	180		
QY	181	HDNICSNGSESTQCGIDVLTCEBAFRFAVPTFTPMWLSVLVDNLTGTVNAESVERI	240		
DB	181	HDNICSNGSESTQCGIDVLTCEBAFRFAVPTFTPMWLSVLVDNLTGTVNAESVERI	240		
QY	241	KRQSSQEQTFQLLKMKHOKKODIYKTIQIDILCBNSVQRIHGANLTFEQLRSIME	300		
DB	241	KRQSSQEQTFQLLKMKHOKKODIYKTIQIDILCBNSVQRIHGANLTFEQLRSIME	300		
QY	301	SLPKYGAEDIEKTIACKRSDOILKLLSLMRKNGDDTLKGLMHALKSKTYHPKXT	360		
DB	301	SLPKYGAEDIEKTIACKRSDOILKLLSLMRKNGDDTLKGLMHALKSKTYHPKXT	360		

Db 301 SLPGKVGADIEDIKTIKACKPSDOIILKLSLWRIKNGDDQTLKGLMHALGHSXYHFPKT 360
QY 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 2

US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PaacSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1

Query Match 100.0%; Score 2200; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3,2e-193;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMT 60
Db 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMT 60
QY 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRSCEPFGVQVAGTBERNTVCKRCPDGFPSNETSSKAPCRKKTNCSVFGLLLTQGNAT 180
Db 121 HRSCEPFGVQVAGTBERNTVCKRCPDGFPSNETSSKAPCRKKTNCSVFGLLLTQGNAT 180
QY 181 HDNIGSGNSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPGTKNAESVERI 240
Db 181 HDNIGSGNSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPGTKNAESVERI 240
QY 241 KROHSSOEOTFOLKLMKHONKQDQIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
Db 241 KROHSSOEOTFOLKLMKHONKQDQIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
QY 301 SLPGKVGADIEDIKTIKACKPSDOIILKLSLWRIKNGDDQTLKGLMHALGHSXYHFPKT 360
Db 301 SLPGKVGADIEDIKTIKACKPSDOIILKLSLWRIKNGDDQTLKGLMHALGHSXYHFPKT 360
QY 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 3

US-10-039-785-5
; Sequence 5, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that immunospecifically bind to TRAIL

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-5

Query Match 100.0%; Score 2200; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3,2e-193;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMT 60
Db 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMT 60
QY 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYLEIEFCLK 120
Db 61 VCAPCPDHYTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRSCEPFGVQVAGTBERNTVCKRCPDGFPSNETSSKAPCRKKTNCSVFGLLLTQGNAT 180
Db 121 HRSCEPFGVQVAGTBERNTVCKRCPDGFPSNETSSKAPCRKKTNCSVFGLLLTQGNAT 180
QY 181 HDNIGSGNSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPGTKNAESVERI 240
Db 181 HDNIGSGNSESTQKCGIDVTLCEBAFFRAVPTKFTPNMLSVLVNLPGTKNAESVERI 240
QY 241 KROHSSOEOTFOLKLMKHONKQDQIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
Db 241 KROHSSOEOTFOLKLMKHONKQDQIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
QY 301 SLPGKVGADIEDIKTIKACKPSDOIILKLSLWRIKNGDDQTLKGLMHALGHSXYHFPKT 360
Db 301 SLPGKVGADIEDIKTIKACKPSDOIILKLSLWRIKNGDDQTLKGLMHALGHSXYHFPKT 360
QY 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
Db 361 VTOSLAKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 4

US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1940 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
ATTORNEY/AGENT INFORMATION:
NAME: Wincer, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-6

Query Match 99.6%; Score 2192; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 1.7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKKKT 60
DB 1 MNKLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKKKT 60
QY 61 VCACPDPHYTDSWHTSDECLYCSPVCKELOYVQKQECNRTNRYVCECKEGRYLEIEFCLK 120
DB 61 VCACPDPHYTDSWHTSDECLYCSPVCKELOYVQKQECNRTNRYVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
DB 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
QY 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
DB 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTVMNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTVMNAESVERI 240
QY 241 KROHSSQEQTFQLKLMGQKQADIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
DB 241 KROHSSQEQTFQLKLMGQKQADIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPEKTVGAEDIETIKACRPSDQILKLSLMRIKNGQDTLKGLMHALKSKTYHPFKT 360
DB 301 SLPEKTVGAEDIETIKACRPSDQILKLSLMRIKNGQDTLKGLMHALKSKTYHPFKT 360
QY 361 VTQSLKKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 5
US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Buefield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-12

Query Match 99.6%; Score 2192; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 1.7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKKKT 60
DB 1 MNKLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCCTAKKKT 60
QY 61 VCACPDPHYTDSWHTSDECLYCSPVCKELOYVQKQECNRTNRYVCECKEGRYLEIEFCLK 120
DB 61 VCACPDPHYTDSWHTSDECLYCSPVCKELOYVQKQECNRTNRYVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
DB 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
QY 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
DB 121 HRSCEPBGVVAQAGTPERNYCKRCPDGFFSNETSARKPCRHNTCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTVMNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLPGTVMNAESVERI 240
QY 241 KROHSSQEQTFQLKLMGQKQADIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
DB 241 KROHSSQEQTFQLKLMGQKQADIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPEKTVGAEDIETIKACRPSDQILKLSLMRIKNGQDTLKGLMHALKSKTYHPFKT 360
DB 301 SLPEKTVGAEDIETIKACRPSDQILKLSLMRIKNGQDTLKGLMHALKSKTYHPFKT 360
QY 361 VTQSLKKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTWYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 6
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.

? APPLICANT: Lacey, David L.
 ? APPLICANT: Calzone, Frank J.
 ? APPLICANT: Chang, Ming-Shi
 ? TITLE OF INVENTION: OSTEOPROTEGERIN
 ? NUMBER OF SEQUENCES: 53
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Amgen Inc.
 ? STREET: 1840 Denavilland Drive
 ? CITY: Thousand Oaks
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 91320-1789
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent in Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/795,445A
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIORITY APPLICATION DATA:
 ? APPLICATION NUMBER: 08/577,788
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Winter, Robert B.
 ? REFERENCE/DOCKET NUMBER: A-378
 ? INFORMATION FOR SEQ ID NO: 6:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 401 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-795-445A-6

Query Match 99.6%; Score 2192; DB 3; Length 401;
 Best Local Similarity 99.8%; Pred. No. 1.7e-192;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBTSQHLCDKCPGTYLKQHTAKMT 60
 DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBTSQHLCDKCPGTYLKQHTAKMT 60
 QY 61 VCAPPCDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTHNRYCECKEGRYLEIEFCLK 120
 DB 61 VCAPPCDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTHNRYCECKEGRYLEIEFCLK 120
 QY 121 HRSCPPGFGVQAGTFRNTVCKRCPDGFPFNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
 DB 121 HRSCPPGFGVQAGTFRNTVCKRCPDGFPFNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
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 DB 181 HDNIGSNGESTQKCGIDVTLCEBAFFRPAVPTKFTNNMLSVLVNDLPGTKVAESVERI 240
 QY 241 KROHSSQEQTFQLLKLMKQNKQDQIVKTIIDIDLCENSVQRIHGHANTTFEQLSLME 300
 DB 241 KROHSSQEQTFQLLKLMKQNKQDQIVKTIIDIDLCENSVQRIHGHANTTFEQLSLME 300
 QY 301 SLPGKVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMALXGSKTYHFPKT 360
 DB 301 SLPGKVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMALXGSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

RESULT 7
 US-08-795-447A-6
 ; Sequence 6, Application US/08795447A
 ; Patent No. 6284728
 ; GENERAL INFORMATION:
 ; APPLICANT: Lacey, David L.

? APPLICANT: Boyle, William J.
 ? APPLICANT: Lacey, David L.
 ? APPLICANT: Calzone, Frank J.
 ? APPLICANT: Chang, Ming-Shi
 ? TITLE OF INVENTION: Osteoprotogerin
 ? NUMBER OF SEQUENCES: 53
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Amgen Inc.
 ? STREET: One Amgen Center Drive
 ? CITY: Thousand Oaks
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 91362-1789
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent in Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/795,447A
 ? FILING DATE:
 ? CLASSIFICATION: 514
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Winter, Robert B.
 ? REFERENCE/DOCKET NUMBER: A-378D2
 ? INFORMATION FOR SEQ ID NO: 6:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 401 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US-08-795-447A-6

Query Match 99.6%; Score 2192; DB 3; Length 401;
 Best Local Similarity 99.8%; Pred. No. 1.7e-192;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBTSQHLCDKCPGTYLKQHTAKMT 60
 DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBTSQHLCDKCPGTYLKQHTAKMT 60
 QY 61 VCAPPCDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTHNRYCECKEGRYLEIEFCLK 120
 DB 61 VCAPPCDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTHNRYCECKEGRYLEIEFCLK 120
 QY 121 HRSCPPGFGVQAGTFRNTVCKRCPDGFPFNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
 DB 121 HRSCPPGFGVQAGTFRNTVCKRCPDGFPFNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
 QY 181 HDNIGSNGESTQKCGIDVTLCEBAFFRPAVPTKFTNNMLSVLVNDLPGTKVAESVERI 240
 DB 181 HDNIGSNGESTQKCGIDVTLCEBAFFRPAVPTKFTNNMLSVLVNDLPGTKVAESVERI 240
 QY 241 KROHSSQEQTFQLLKLMKQNKQDQIVKTIIDIDLCENSVQRIHGHANTTFEQLSLME 300
 DB 241 KROHSSQEQTFQLLKLMKQNKQDQIVKTIIDIDLCENSVQRIHGHANTTFEQLSLME 300
 QY 301 SLPGKVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMALXGSKTYHFPKT 360
 DB 301 SLPGKVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMALXGSKTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

RESULT 8
 US-08-974-186-6
 ; Sequence 6, Application US/08974186
 ; Patent No. 6284740
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-6

Query Match 99.6%; Score 2192; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 1.7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCYAKWKT 60
DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCYAKWKT 60
QY 61 VCAPCPDHYTDSWHTSDECLYCSPVCKELOYVQECNRTNRCVCEKGRYLEIEFCLK 120
DB 61 VCAPCPDHYTDSWHTSDECLYCSPVCKELOYVQECNRTNRCVCEKGRYLEIEFCLK 120
QY 121 HRSCPGFQVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCPGFQVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTOKCGIDVTLCBEAFPRFAVPTKFTPMWLSVLVDNLPGTKVNAESVERI 240
DB 181 HDNICSNGSESTOKCGIDVTLCBEAFPRFAVPTKFTPMWLSVLVDNLPGTKVNAESVERI 240
QY 241 KROHSSQEQFTQLKLMGHQNKADIVKTIIDIDLCENSVQRHIGHANLTFEOLRSIME 300
DB 241 KROHSSQEQFTQLKLMGHQNKADIVKTIIDIDLCENSVQRHIGHANLTFEOLRSIME 300
QY 301 SLPGKVGAEADIEKTIKACRPSDQILKLSLMRIKNGDQDTLKGIMHALKHSKTYHPFKT 360
DB 301 SLPGKVGAEADIEKTIKACRPSDQILKLSLMRIKNGDQDTLKGIMHALKHSKTYHPFKT 360
QY 361 VTOSLKTIRFLHSFTMYKLYQKLFLEWIGNOVOSVKISCL 401
DB 361 VTOSLKTIRFLHSFTMYKLYQKLFLEWIGNOVOSVKISCL 401

RESULT 9
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-6

Query Match 99.6%; Score 2192; DB 3; Length 401;
Best Local Similarity 99.8%; Pred. No. 1.7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCYAKWKT 60
DB 1 MNKLCCALVFLDISIKMTTQETFPKYLHYDEETSHQLCDKCPGTYLKQHCYAKWKT 60
QY 61 VCAPCPDHYTDSWHTSDECLYCSPVCKELOYVQECNRTNRCVCEKGRYLEIEFCLK 120
DB 61 VCAPCPDHYTDSWHTSDECLYCSPVCKELOYVQECNRTNRCVCEKGRYLEIEFCLK 120
QY 121 HRSCPGFQVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCPGFQVQAGTPERNIVCKRCPDGFNSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTOKCGIDVTLCBEAFPRFAVPTKFTPMWLSVLVDNLPGTKVNAESVERI 240
DB 181 HDNICSNGSESTOKCGIDVTLCBEAFPRFAVPTKFTPMWLSVLVDNLPGTKVNAESVERI 240
QY 241 KROHSSQEQFTQLKLMGHQNKADIVKTIIDIDLCENSVQRHIGHANLTFEOLRSIME 300
DB 241 KROHSSQEQFTQLKLMGHQNKADIVKTIIDIDLCENSVQRHIGHANLTFEOLRSIME 300
QY 301 SLPGKVGAEADIEKTIKACRPSDQILKLSLMRIKNGDQDTLKGIMHALKHSKTYHPFKT 360
DB 301 SLPGKVGAEADIEKTIKACRPSDQILKLSLMRIKNGDQDTLKGIMHALKHSKTYHPFKT 360
QY 361 VTOSLKTIRFLHSFTMYKLYQKLFLEWIGNOVOSVKISCL 401
DB 361 VTOSLKTIRFLHSFTMYKLYQKLFLEWIGNOVOSVKISCL 401

RESULT 10
US-08-706-945D-128
; Sequence 128, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:

; APPLICANT: Boyle, William
 ; APPLICANT: Lacey, David
 ; APPLICANT: Calzone, Frank
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: Osteoprotegerin
 ; FILE REFERENCE: A-378CIP
 ; CURRENT APPLICATION NUMBER: US/08/706,945D
 ; CURRENT FILING DATE: 1996-09-03
 ; PRIOR APPLICATION NUMBER: 08/577,788
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 145
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 128
 ; LENGTH: 401
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 ; US-08-706-945D-128

Query Match 99.6%; Score 2192; DB 4; Length 401;

Best Local Similarity 99.8%; Pred. No. 1,7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 QY 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 DB 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 QY 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240
 DB 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240
 QY 241 KROHSSQEQTFOLKLMKHQNKQADIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
 DB 241 KROHSSQEQTFOLKLMKHQNKQADIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
 QY 301 SLPGKRVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALKHSTYHPKPT 360
 DB 301 SLPGKRVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALKHSTYHPKPT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 11

; US-08-577-788C-6
 ; Sequence 6, Application US/08577788C
 ; Patent No. 6613544
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William
 ; APPLICANT: Lacey, David
 ; APPLICANT: Calzone, Frank
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: Osteoprotegerin
 ; FILE REFERENCE: A-378 Rev
 ; CURRENT APPLICATION NUMBER: US/08/577,788C
 ; CURRENT FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 401
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 ; US-08-577-788C-6

Query Match 99.6%; Score 2192; DB 4; Length 401;

Best Local Similarity 99.8%; Pred. No. 1,7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 QY 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 DB 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 QY 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240
 DB 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240
 QY 241 KROHSSQEQTFOLKLMKHQNKQADIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
 DB 241 KROHSSQEQTFOLKLMKHQNKQADIVKTIIDIDICENSVOHIGHANLTFEQLSLME 300
 QY 301 SLPGKRVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALKHSTYHPKPT 360
 DB 301 SLPGKRVGADIEKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALKHSTYHPKPT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYOKLFLEMIGNOVQSVKISCL 401

RESULT 12

; US-08-577-788C-56
 ; Sequence 56, Application US/08577788C
 ; Patent No. 6613544
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William
 ; APPLICANT: Lacey, David
 ; APPLICANT: Calzone, Frank
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: Osteoprotegerin
 ; FILE REFERENCE: A-378 Rev
 ; CURRENT APPLICATION NUMBER: US/08/577,788C
 ; CURRENT FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 56
 ; LENGTH: 401
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 ; US-08-577-788C-56

Query Match 99.6%; Score 2192; DB 4; Length 401;
Best Local Similarity 99.8%; Pred. No. 1,7e-192;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 DB 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDEBESHQLLCDKCPGTYLKQCHTAKMKT 60
 QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVQKQECNTHNRCVCEKGRYLEIEFCLK 120
 QY 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 DB 121 HSCPPGFGVQAGTBERNTVCRCRCPDGFPSNETSSKAPCRKKTNCVFGLLLTOKGNAT 180
 QY 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240
 DB 181 HDNIGSGNSESTOKCGIDVTLCBEAFRFAVPKFTPNMLSVLVNDLPGRKVAESVERI 240

Qy 241 KROHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 300
 Db 241 KROHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 300
 Qy 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKT 360
 Db 301 SLPGKVGAEIDIEKTIKACRPSDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKT 360
 Qy 361 VTOSLTKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
 Db 361 VTOSLTKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 13
 US-08-706-945D-142
 ; Sequence 142; Application US/08706945D
 ; Patent No. 6369027
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William
 ; APPLICANT: Lacey, David
 ; APPLICANT: Calzone, Frank
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: Osteoprotegerin
 ; FILE REFERENCE: A-378CIP
 ; CURRENT APPLICATION NUMBER: US/08/706,945D
 ; CURRENT FILING DATE: 1996-09-03
 ; PRIOR APPLICATION NUMBER: 08/577,788
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 145
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 142
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-08-706-945D-142

Query Match 89.8%; Score 1976; DB 4; Length 364;
 Best Local Similarity 95.5%; Pred. No. 9,2e-173;
 Matches 363; Conservative 0; Mismatches 1; Indels 16; Gaps 1;
 Qy 22 ETFFPKYLHYDEETSHQLLCDKCPRTYLYKQHTAKMKTVCAPCPDHYTDSMHTSDECL 81
 Db 1 ETFFPKYLHYDEETSHQLLCDKCPRTYLYKQHTAKMKTVCAPCPDHYTDSMHTSDECL 60
 Qy 82 YCSVVCCELQYVKEQCNRTNHRVCECKEGRYLEIFCLKHSCEPGEVVOAGTPEBRTV 141
 Db 61 YCSVVCCELQYVKEQCNRTNHRVCECKEGRYLEIFCLKHSCEPGEVVOAGTPEBRTV 120
 Qy 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKGIDVTL 201
 Db 121 CKRCPDGFSSNETSSKAPCRKHTN-----DNICSGNSESTOKGIDVTL 164
 Qy 202 CEEAFPRFVAVPTKFTPNMLSVLVNLPPTKYNAESVERIKROHSSOBTQOLKLMKQKON 261
 Db 165 CEEAFPRFVAVPTKFTPNMLSVLVNLPPTKYNAESVERIKROHSSOBTQOLKLMKQKON 224
 Qy 262 KDOQIVKIIIDIDLCENSVOHIGHANLTFEOLRLMESLPKGVGAEDIEKTIKACR 321
 Db 225 KAOQIVKIIIDIDLCENSVOHIGHANLTFEOLRLMESLPKGVGAEDIEKTIKACR 284
 Qy 322 SDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKTIRFLHSFTMYKLY 381
 Db 285 SDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKTIRFLHSFTMYKLY 344
 Qy 382 OKLFLEMIGNOVOSVKISCL 401
 Db 345 OKLFLEMIGNOVOSVKISCL 364

RESULT 14
 US-08-974-022-2
 ; Sequence 2; Application US/08974022
 ; Patent No. 6015938

GENERAL INFORMATION:
 APPLICANT: Boyle, William J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1640 Denavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,022
 FILING DATE: 12-DEC-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/577,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wincer, Robert B.
 REFERENCE/DOCKET NUMBER: A-378
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-974-022-2

Query Match 87.0%; Score 1914; DB 3; Length 401;
 Best Local Similarity 86.3%; Pred. No. 5e-167;
 Matches 347; Conservative 25; Mismatches 28; Indels 2; Gaps 2;
 Qy 1 MNKLCCA-LVFLDISIKMTQETFPKYLHYDEETSHQLLCDKCPRTYLYKQHTAKMK 59
 Db 1 MNKLCCALLVFLDI-LEMTTOETFPKYLHYDEETSHQLLCDKCAPRTYLYKQHTAKRK 59
 Qy 60 TVCAPCPDHYTDSMHTSDECLYCSVVCCELQYVKEQCNRTNHRVCECKEGRYLEIFCL 119
 Db 60 TVCAPCPDHYTDSMHTSDECLYCSVVCCELQYVKEQCNRTNHRVCECKEGRYLEIFCL 119
 Qy 120 KHRSCPRFQVVOAGTPEBRTNVCRCRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
 Db 120 KHRSCPRFQVVOAGTPEBRTNVCRCRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
 Qy 120 KHRSCPRFQVVOAGTPEBRTNVCRCRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
 Db 120 KHRSCPRFQVVOAGTPEBRTNVCRCRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179
 Qy 180 THDNICSGNSESTOKGIDVTLCEEAFPRFVAVPTKFTPNMLSVLVNLPPTKYNAESVER 239
 Db 180 THDNICSGNSESTOKGIDVTLCEEAFPRFVAVPTKFTPNMLSVLVNLPPTKYNAESVER 239
 Qy 240 IKROHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 299
 Db 240 IKROHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 299
 Qy 240 IKRHHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 299
 Db 240 IKRHHSSOBTQOLKLMKQKNDODIVKIIIDIDLCENSVOHIGHANLTFEOLRLME 299
 Qy 300 ESLPGKVGAEIDIEKTIKACRPSDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKT 359
 Db 300 ESLPGKVGAEIDIEKTIKACRPSDQILKLSLWRKNGDQDITLKGMLHAKSKTYHPEKT 359
 Qy 360 TVTOSLTKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401
 Db 360 TVTOSLTKTIRFLHSFTMYKLYOKLFLEMIGNOVOSVKISCL 401

RESULT 15
 US-08-795-445A-2
 ; Sequence 2; Application US/08795445A

Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-2

Query Match 87.0%; Score 1914; DB 3; Length 401;
Best Local Similarity 86.3%; Pred. No. 5e-167;
Matches 347; Conservative 25; Mismatches 28; Indels 2; Gaps 2;

QY 1 MNKLLCA-LVFLDISIKMTTOETFPKYLHYDETSNOLLCDCPPTGLKOHCTAKWK 59
DB 1 MNKMLCCALLVFLDI-LEWTTQETFFPKYLHYDETRQLLDCXCAPGYLKHCTVARK 59
QY 60 TVCAPCPDHAYTDSMTSDCLYCSPIYCKELQYVKQECNRTNHRVCECKEGRYLEIFCL 119
DB 60 TLCPVCPDYSYTDSTWHTSDSCVYCSPIYCKELQYVKQECNRTNHRVCECKEGRYLEIFCL 119
QY 120 KHRSCPPGFGVVOAGTPEBNTVCKRCPCDGFPSNETSSKAPCRKHTNCSVGLLLTOKGNA 179
DB 120 KHRSCPPGLGLVLOAGTPEBNTVCKRCPCDGFPSNETSSKAPCRKHTNCSVGLLLTOKGNA 179
QY 180 THDNICSGNSESIOKCGIDVTLCEAFPRPAVPTKFTPNWLSVLDNLPGTKVNASVER 239
DB 180 THDNVCGNBEATQNGCIDVTLCEAFPRPAVPTKFTPNWLSVLDNLPGTKVNASVER 239
QY 240 IKRQHSQEQOTFOLLKMKQONKQDIYKIIIDIDILCENSVOHIGHANULTFEQLSLM 299
DB 240 IKRHSQEQOTFOLLKMKQONKQDIYKIIIDIDILCENSVOHIGHANULTFEQLSLM 299
QY 300 ESLPGKVGADIEKTKACKPSDQILKLSIMRIKNGDDTLKGLMHALKHSTYHFPK 359
DB 300 ESLPGKGISPELERTKTCPSQQLKLSLWRIKNGDDTLKGLMYALKHLKAYHFPK 359
QY 360 TVTQSLAKTIRFLHSFTMYKLYQKLFLEMIGNQVSVKISCL 401
DB 360 TVTHTSLAKTIRFLHSFTMYRLYQKLFLEMIGNQVSVKISCL 401

Search completed: September 29, 2004, 12:35:02
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 12:32:12 ; Search time 133 Seconds
(without alignment)
970.237 Million cell updates/sec

Title: US-09-526-437-2

Perfect score: 2200

Sequence: 1 MNKLLCCALVFLDISIKWT.....OKLFLEMIGNQVSKISCL 401

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications_AA:*

2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2200	100.0	401	12	US-10-105-934-2
2	2200	100.0	401	13	US-10-039-785-5
3	2200	100.0	401	13	US-10-066-209-1
4	2200	100.0	401	13	US-10-164-592-2
5	2200	100.0	401	14	US-10-044-674-3
6	2200	100.0	401	14	US-10-322-673-5
7	2200	100.0	401	14	US-10-139-785-5
8	2195	99.8	401	9	US-09-062-113-5
9	2195	99.8	401	14	US-10-183-091-1
10	2195	99.8	401	14	US-10-364-045-1
11	2195	99.8	401	14	US-10-232-858-5
12	2195	99.8	401	15	US-10-377-076-1
13	2195	99.8	401	16	US-10-785-109-5
14	2195	99.8	401	16	US-10-785-114-5
15	2192	99.6	401	11	US-09-405-032-125

16	2192	99.6	401	12	US-10-151-071-8	Sequence 8, Appli
17	2192	99.6	401	16	US-10-467-243-2	Sequence 2, Appli
18	2187	99.4	400	14	US-10-142-658-2	Sequence 2, Appli
19	2185	99.3	401	9	US-09-062-113-62	Sequence 62, Appli
20	2185	99.3	401	9	US-09-062-113-63	Sequence 63, Appli
21	2185	99.3	401	9	US-09-062-113-64	Sequence 64, Appli
22	2185	99.3	401	9	US-09-062-113-65	Sequence 65, Appli
23	2185	99.3	401	9	US-09-062-113-66	Sequence 66, Appli
24	2185	99.3	401	14	US-10-232-858-62	Sequence 62, Appli
25	2185	99.3	401	14	US-10-232-858-63	Sequence 63, Appli
26	2185	99.3	401	14	US-10-232-858-64	Sequence 64, Appli
27	2185	99.3	401	14	US-10-232-858-65	Sequence 65, Appli
28	2185	99.3	401	14	US-10-232-858-66	Sequence 66, Appli
29	2185	99.3	401	16	US-10-785-109-62	Sequence 62, Appli
30	2185	99.3	401	16	US-10-785-109-63	Sequence 63, Appli
31	2185	99.3	401	16	US-10-785-109-64	Sequence 64, Appli
32	2185	99.3	401	16	US-10-785-109-65	Sequence 65, Appli
33	2185	99.3	401	16	US-10-785-109-66	Sequence 66, Appli
34	2185	99.3	401	16	US-10-785-114-62	Sequence 62, Appli
35	2185	99.3	401	16	US-10-785-114-63	Sequence 63, Appli
36	2185	99.3	401	16	US-10-785-114-64	Sequence 64, Appli
37	2185	99.3	401	16	US-10-785-114-65	Sequence 65, Appli
38	2185	99.3	401	16	US-10-785-114-66	Sequence 66, Appli
39	2182	99.2	399	9	US-09-062-113-73	Sequence 73, Appli
40	2182	99.2	399	14	US-10-232-858-73	Sequence 73, Appli
41	2182	99.2	399	16	US-10-785-109-73	Sequence 73, Appli
42	2182	99.2	399	16	US-10-785-114-73	Sequence 73, Appli
43	2149	97.7	393	9	US-09-062-113-79	Sequence 79, Appli
44	2149	97.7	393	14	US-10-232-858-79	Sequence 79, Appli
45	2149	97.7	393	16	US-10-785-109-79	Sequence 79, Appli

ALIGNMENTS

RESULT 1

US-10-105-934-2

Sequence 2, Application US/10105934

Publication No. US20020150988A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

Holtzman, Douglas

TITLE OF INVENTION: NOVEL MOLECULES OF THE FTHMA-070-RELATED PROTEIN FAMILY AND USES THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/105,934

FILING DATE: 25-Mar-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/062,389

FILING DATE: 17-Apr-1998

APPLICATION NUMBER: 60/062,017

FILING DATE: 10-Oct-1997

APPLICATION NUMBER: 60/044,746

FILING DATE: 18-Apr-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weikiejohn, Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 09404/051001

TELECOMMUNICATION INFORMATION:

```

/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 401 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-105-934-2

Query Match      100.0%; Score 2200; DB 12; Length 401;
Best Local Similarity 100.0%; Pred. No. 8,2e-178;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGTYLKQCHTAKMT 60
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DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVKBQCNRTNHNVCCEKGRYLEIEFCIK 120
QY 121 HRACPPGFGVQAGTPEERNTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKNAT 180
DB 121 HRACPPGFGVQAGTPEERNTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKNAT 180
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DB 181 HDNICSNSSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSVLVNLPGTKVNAESVERI 240
QY 241 KRQSSQEQTFOLLKLMKQNKQDQIVKKIIQDIDLCEVSVQRHIGHANLTFEQLSLME 300
DB 241 KRQSSQEQTFOLLKLMKQNKQDQIVKKIIQDIDLCEVSVQRHIGHANLTFEQLSLME 300
QY 301 SLPGKVGADIEDIKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALGHSKTYHPKPT 360
DB 301 SLPGKVGADIEDIKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALGHSKTYHPKPT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 2
US-10-039-785-5
/ Sequence 5, Application US/10039785
/ Publication No. US2002067646A1
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ FILE REFERENCE: PFS50
/ CURRENT APPLICATION NUMBER: US/10/039, 785
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,176
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04

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/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-039-785-5

Query Match      100.0%; Score 2200; DB 13; Length 401;
Best Local Similarity 100.0%; Pred. No. 8,2e-178;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGTYLKQCHTAKMT 60
DB 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEETSHQLCDKCPGTYLKQCHTAKMT 60
QY 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVKBQCNRTNHNVCCEKGRYLEIEFCIK 120
DB 61 VCAPCPDHYTDSMHTSDECLYCSPVCKELQYVKBQCNRTNHNVCCEKGRYLEIEFCIK 120
QY 121 HRACPPGFGVQAGTPEERNTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKNAT 180
DB 121 HRACPPGFGVQAGTPEERNTVCKRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKNAT 180
QY 181 HDNICSNSSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSVLVNLPGTKVNAESVERI 240
DB 181 HDNICSNSSESTQKCGIDVTLCBEAFPRFAVPTKFTPNMLSVLVNLPGTKVNAESVERI 240
QY 241 KRQSSQEQTFOLLKLMKQNKQDQIVKKIIQDIDLCEVSVQRHIGHANLTFEQLSLME 300
DB 241 KRQSSQEQTFOLLKLMKQNKQDQIVKKIIQDIDLCEVSVQRHIGHANLTFEQLSLME 300
QY 301 SLPGKVGADIEDIKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALGHSKTYHPKPT 360
DB 301 SLPGKVGADIEDIKTIKACKPSDQILKLSLWRIKNGDQDTLGLMHALGHSKTYHPKPT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3
US-10-066-209-1
/ Sequence 1, Application US/10066209
/ Publication No. US20020115110A1
/ GENERAL INFORMATION:
/ APPLICANT: Brigham-Burke, Michael R.
/ APPLICANT: Young, Peter R.
/ TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
/ TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
/ FILE REFERENCE: GH-50030-D1
/ CURRENT APPLICATION NUMBER: US/10/066, 209
/ PRIOR FILING DATE: 2001-10-25
/ PRIOR APPLICATION NUMBER: 09/072,993
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/055,513
/ PRIOR FILING DATE: 1997-08-13
/ PRIOR APPLICATION NUMBER: 60/056,980
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/057,550
/ PRIOR FILING DATE: 1997-08-29
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: HOMO SAPIENS
US-10-066-209-1

Query Match      100.0%; Score 2200; DB 13; Length 401;
Best Local Similarity 100.0%; Pred. No. 8,2e-178;

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Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLLCALVFLDISIKMTTQETFPKYLHYDEETSHOLLCDKCPGTYLKQHTAKMKT 60
 DB 1 MNKLLCALVFLDISIKMTTQETFPKYLHYDEETSHOLLCDKCPGTYLKQHTAKMKT 60

QY 61 VCAPCPDHYTDSMTSDECLYCSVCKELQYVQECNRTNHRVCECKEGRYLIEFCLK 120
 DB 61 VCAPCPDHYTDSMTSDECLYCSVCKELQYVQECNRTNHRVCECKEGRYLIEFCLK 120

QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
 DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180

QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLTGTVMNESVERI 240
 DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLTGTVMNESVERI 240

QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 4
 US-10-164-592-2
 ; Sequence 2, Application US/10164592
 ; Publication No. US20020150989A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, John M.
 ; APPLICANT: Fleischmann, Robert D.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
 ; FILE REFERENCE: 1488.0710007
 ; CURRENT APPLICATION NUMBER: US/10/164.592
 ; PRIOR FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: US 08/469,637
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: PCT/US95/03216
 ; PRIOR FILING DATE: 1995-03-15
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-164-592-2

Query Match 100.0%; Score 2200; DB 13; Length 401;
 Best Local Similarity 100.0%; Pred. No. 8.2e-178;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 KROHSSQOTFQLKLMHGONKODIVKIIODIDLGENSVQRHIGHANLTFEQLSLME 300
 DB 241 KROHSSQOTFQLKLMHGONKODIVKIIODIDLGENSVQRHIGHANLTFEQLSLME 300

QY 301 SLPGKKGABDIETIKAKCPSPDQILKLSLMRIRNGQDITLKGIMHALKHSKTYHPKXT 360
 DB 301 SLPGKKGABDIETIKAKCPSPDQILKLSLMRIRNGQDITLKGIMHALKHSKTYHPKXT 360

QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 5
 US-10-044-674-3
 ; Sequence 3, Application US/10044674
 ; Publication No. US20030175710A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Denton, R. Rex
 ; APPLICANT: Bieglecki, Karyn M
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Stephens, J. Claiborne
 ; TITLE OF INVENTION: HAPLOYPES OF THE TNFRSF1B GENE
 ; FILE REFERENCE: TNFRSF1B MMH-0001US (CIP)
 ; CURRENT APPLICATION NUMBER: US/10/044.674
 ; PRIOR FILING DATE: 2002-01-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/18803
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 94
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-044-674-3

Query Match 100.0%; Score 2200; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 8.2e-178;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MNKLLCALVFLDISIKMTTQETFPKYLHYDEETSHOLLCDKCPGTYLKQHTAKMKT 60

QY 61 VCAPCPDHYTDSMTSDECLYCSVCKELQYVQECNRTNHRVCECKEGRYLIEFCLK 120
 DB 61 VCAPCPDHYTDSMTSDECLYCSVCKELQYVQECNRTNHRVCECKEGRYLIEFCLK 120

QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
 DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180

QY 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLTGTVMNESVERI 240
 DB 181 HDNICSNGSESTQKCGIDVTLCCEAFPRFAVPTKFTPMWLSVLDNLTGTVMNESVERI 240

QY 241 KROHSSQOTFQLKLMHGONKODIVKIIODIDLGENSVQRHIGHANLTFEQLSLME 300
 DB 241 KROHSSQOTFQLKLMHGONKODIVKIIODIDLGENSVQRHIGHANLTFEQLSLME 300

QY 301 SLPGKKGABDIETIKAKCPSPDQILKLSLMRIRNGQDITLKGIMHALKHSKTYHPKXT 360
 DB 301 SLPGKKGABDIETIKAKCPSPDQILKLSLMRIRNGQDITLKGIMHALKHSKTYHPKXT 360

QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401
 DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 6
 US-10-322-673-5

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/ Sequence 5, Application US/10322673
/ Publication No. US20030180296A1
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ FILE REFERENCE: PF585
/ CURRENT APPLICATION NUMBER: US/10/322,673
/ PRIOR FILING DATE: 2002-12-19
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/369,877
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/384,828
/ PRIOR FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/396,591
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/403,370
/ PRIOR FILING DATE: 2002-08-15
/ PRIOR APPLICATION NUMBER: 60/425,737
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 72
/ SEQ ID NO 5
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-322-673-5

Query Match      100.0%; Score 2200; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.2e-178;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MNKLCCALVFLDISIKMTQETFPKYLHYDETSHQLLCDKCPGTLYKHQCTAKMT 60
DB 1 MNKLCCALVFLDISIKMTQETFPKYLHYDETSHQLLCDKCPGTLYKHQCTAKMT 60
QY 61 VCAPCPDHYTSDWHTSDECLYCSPVCKELQYVQKQCNRTNHNVCCKEGRYLEIEFCLK 120
DB 61 VCAPCPDHYTSDWHTSDECLYCSPVCKELQYVQKQCNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRSCPFGVQVQAGTPEPRNTVCRCRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCPFGVQVQAGTPEPRNTVCRCRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNSSESTQKCGIDVTLCEAPFRFAVPTKFTPNMWSLVLDNLPGTKVNAESVERI 240
DB 181 HDNICSNSSESTQKCGIDVTLCEAPFRFAVPTKFTPNMWSLVLDNLPGTKVNAESVERI 240
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DB 241 KRQSSQEQTFOLLKLMKQNKQDQIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPGKRVGAEIDIEKTIKACRPSDQILKLSLWRIKNGDQDTLKGMLALKHSKTYHPKXT 360
DB 301 SLPGKRVGAEIDIEKTIKACRPSDQILKLSLWRIKNGDQDTLKGMLALKHSKTYHPKXT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401
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RESULT 7
US-10-139-785-5
/ Sequence 5, Application US/10139785
/ Publication No. US20030190685A1
/ GENERAL INFORMATION:
/ APPLICANT: Salcedo et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ FILE REFERENCE: PF550
/ CURRENT APPLICATION NUMBER: US/10/139,785
/ PRIOR APPLICATION NUMBER: 60/369,860
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/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,176
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-139-785-5

Query Match      100.0%; Score 2200; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.2e-178;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MNKLCCALVFLDISIKMTQETFPKYLHYDETSHQLLCDKCPGTLYKHQCTAKMT 60
DB 1 MNKLCCALVFLDISIKMTQETFPKYLHYDETSHQLLCDKCPGTLYKHQCTAKMT 60
QY 61 VCAPCPDHYTSDWHTSDECLYCSPVCKELQYVQKQCNRTNHNVCCKEGRYLEIEFCLK 120
DB 61 VCAPCPDHYTSDWHTSDECLYCSPVCKELQYVQKQCNRTNHNVCCKEGRYLEIEFCLK 120
QY 121 HRSCPFGVQVQAGTPEPRNTVCRCRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCPFGVQVQAGTPEPRNTVCRCRCPDGFPSNETSSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNSSESTQKCGIDVTLCEAPFRFAVPTKFTPNMWSLVLDNLPGTKVNAESVERI 240
DB 181 HDNICSNSSESTQKCGIDVTLCEAPFRFAVPTKFTPNMWSLVLDNLPGTKVNAESVERI 240
QY 241 KRQSSQEQTFOLLKLMKQNKQDQIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
DB 241 KRQSSQEQTFOLLKLMKQNKQDQIVKIIQDIDLCENSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPGKRVGAEIDIEKTIKACRPSDQILKLSLWRIKNGDQDTLKGMLALKHSKTYHPKXT 360
DB 301 SLPGKRVGAEIDIEKTIKACRPSDQILKLSLWRIKNGDQDTLKGMLALKHSKTYHPKXT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVSVKISCL 401
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RESULT 8
US-09-062-113-5
/ Sequence 5, Application US/09062113
/ Patent No. US20020051969A1
/ GENERAL INFORMATION:
/ APPLICANT: GOTO, Masaki
/ APPLICANT: TSUDA, Eisuke
/ APPLICANT: MOCHIZUKI, Shin'ichi
/ APPLICANT: YANO, Kazuki
/ APPLICANT: KOBAYASHI, Fumie
/ APPLICANT: SHIMA, No. US20020051969A1uyuki
/ APPLICANT: YASUDA, Hisataka
/ APPLICANT: NAKAGAWA, No. US20020051969A1uaki
/ APPLICANT: MORINAGA, Tomonori
/ APPLICANT: UEDA, Masatsugu
```

APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1e1 Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Teeba, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..380
OTHER INFORMATION: /note= "(OCIF protein)"
FEATURE:
NAME/KEY: Peptide
LOCATION: -21..0
OTHER INFORMATION: /note= "(signal peptide)"
US-09-062-113-5
Query Match 99.8%; Score 2195; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 2.2e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKWTQETFPKYLHDEBTSQLLCDKCPGGTYLKHQCTAKKKT 60
DB 1 MNKLCCALVFLDISIKWTQETFPKYLHDEBTSQLLCDKCPGGTYLKHQCTAKKKT 60
QY 61 VCACPCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYVCECKEGRYLEIEFCLK 120
DB 61 VCACPCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPGGVVQAGTPERNVTCRCPCPDGFFSNETSAPKCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPERNVTCRCPCPDGFFSNETSAPKCRKHTNCSVFGLLLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPMWLSVLDNLPGTVMASVERI 240

DB 181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPMWLSVLDNLPGTVMASVERI 240
QY 241 KRQSSQECTPOLKLMKQKNDQDIYKKIIDDLCNSVGRHGHANLTQEURSLME 300
DB 241 KRQSSQECTPOLKLMKQKNDQDIYKKIIDDLCNSVGRHGHANLTQEURSLME 300
QY 301 SLPGKKVGADEDEKTKACPSDQILKLSLWRKNGODTLKGLMHLKSKTHFPKT 360
DB 301 SLPGKKVGADEDEKTKACPSDQILKLSLWRKNGODTLKGLMHLKSKTHFPKT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
RESULT 9
US-10-183-091-1
Sequence 1, Application US/10183091
Publication No. US20030045456A1
GENERAL INFORMATION:
APPLICANT: Yamamoto, Shinichi
APPLICANT: Okada, Junichi
APPLICANT: Kurihara, Atsushi
APPLICANT: Numazawa, Taku
APPLICANT: Kondo, Junichi Tsuda, Eisuke
APPLICANT: Mochizuki, Shinichi
APPLICANT: Niimi, Hirotsuka
APPLICANT: Miyazaki, Hideki
TITLE OF INVENTION: A complex comprising OCIF and polysaccharide
FILE REFERENCE: 02280/HG
CURRENT FILING DATE: 2002-06-27
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (-21)..(-1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat peptide
LOCATION: (+1)..(+380)
OTHER INFORMATION:
US-10-183-091-1
Query Match 99.8%; Score 2195; DB 14; Length 401;
Best Local Similarity 99.8%; Pred. No. 2.2e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKWTQETFPKYLHDEBTSQLLCDKCPGGTYLKHQCTAKKKT 60
DB 1 MNKLCCALVFLDISIKWTQETFPKYLHDEBTSQLLCDKCPGGTYLKHQCTAKKKT 60
QY 61 VCACPCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYVCECKEGRYLEIEFCLK 120
DB 61 VCACPCPDHYTDSWHTSDECLYCSPVCKELQYVQECNRTNRYVCECKEGRYLEIEFCLK 120
QY 121 HRSCEPGGVVQAGTPERNVTCRCPCPDGFFSNETSAPKCRKHTNCSVFGLLLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPERNVTCRCPCPDGFFSNETSAPKCRKHTNCSVFGLLLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPMWLSVLDNLPGTVMASVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCEBAFFRAVPTKFTPMWLSVLDNLPGTVMASVERI 240
QY 241 KRQSSQECTPOLKLMKQKNDQDIYKKIIDDLCNSVGRHGHANLTQEURSLME 300

Db 241 KRQHSQEQTFQLLKLMKQNKDQIVKKIIDDIDLCENSVOHRIHGANLTFEQLSLME 300
 QY 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 Db 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 10

US-10-364-045-1
 ; Sequence 1, Application US/10364045
 ; Publication No. US20030139325A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamamoto, Shinichi
 ; APPLICANT: Okada, Junichi
 ; APPLICANT: Kurihara, Akeushi
 ; APPLICANT: Numazawa, Taku
 ; APPLICANT: Kondo, Junichi Tsuda, Eisuke
 ; APPLICANT: Mochizuki, Shinichi
 ; APPLICANT: Nishi, Hirotaka
 ; APPLICANT: Miyazaki, Hideki
 ; TITLE OF INVENTION: A complex comprising OCIF and polysaccharide
 ; FILE REFERENCE: 02280/HG
 ; CURRENT APPLICATION NUMBER: US/10/364,045
 ; CURRENT FILING DATE: 2003-02-11
 ; PRIOR APPLICATION NUMBER: US/10/183,091
 ; PRIOR FILING DATE: 2002-06-27
 ; PRIOR APPLICATION NUMBER: JP 2001-198985
 ; PRIOR FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (-21)..(-1)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: (+1)..(+380)
 ; OTHER INFORMATION:
 ; US-10-364-045-1

Query Match 99.8%; Score 2195; DB 14; Length 401;
 Best Local Similarity 99.8%; Pred. No. 2,2e-177;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDETSQHLCDKCPGTYLKQHTAKMT 60
 Db 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDETSQHLCDKCPGTYLKQHTAKMT 60
 QY 61 VCAPCPDHYVTDSMHTSDECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 Db 61 VCAPCPDHYVTDSMHTSDECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 QY 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 Db 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 QY 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 Db 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 QY 181 HDNICGNSSTQKCGIDVTLCBEAFPRFAVPTKFTPMNLVAVDNLPGTKVNAESVERI 240
 Db 181 HDNICGNSSTQKCGIDVTLCBEAFPRFAVPTKFTPMNLVAVDNLPGTKVNAESVERI 240
 QY 241 KRQHSQEQTFQLLKLMKQNKDQIVKKIIDDIDLCENSVOHRIHGANLTFEQLSLME 300
 Db 241 KRQHSQEQTFQLLKLMKQNKDQIVKKIIDDIDLCENSVOHRIHGANLTFEQLSLME 300
 QY 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 Db 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360

Db 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 11

US-10-232-858-5
 ; Sequence 5, Application US/10232858
 ; Publication No. US20030153048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOTO, Masaaki
 ; APPLICANT: TSUDA, Eisuke
 ; APPLICANT: MOCHIZUKI, Shin'ichi
 ; APPLICANT: YANO, Kazuki
 ; APPLICANT: KOBAYASHI, Fumie
 ; APPLICANT: SHIMA, No. US20030153048A1uyuk1
 ; APPLICANT: YASUDA, Hirotaka
 ; APPLICANT: NAKAGAWA, No. US20030153048A1uaki
 ; APPLICANT: MORINAGA, Tomonori
 ; APPLICANT: UEDA, Masaeugu
 ; TITLE OF INVENTION: No. US20030153048A1e1 Proteins and Methods for Producing the Prote
 ; FILE REFERENCE: 16991.004
 ; CURRENT APPLICATION NUMBER: US/10/232,858
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: PCT/JP96/00374
 ; PRIOR FILING DATE: 1996-02-20
 ; PRIOR APPLICATION NUMBER: 08/915,004
 ; PRIOR FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 401
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-232-858-5

Query Match 99.8%; Score 2195; DB 14; Length 401;
 Best Local Similarity 99.8%; Pred. No. 2,2e-177;
 Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDETSQHLCDKCPGTYLKQHTAKMT 60
 Db 1 MNKLCCALVFLDISIKMTTOETFPKYLHYDETSQHLCDKCPGTYLKQHTAKMT 60
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 Db 61 VCAPCPDHYVTDSMHTSDECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLK 120
 QY 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 Db 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 QY 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 Db 121 HRSCTPGFGVQAQGTBERNTVCKRCPDGFPSNETSSKAPCRKATNCSVFGLLLTQKNAT 180
 QY 181 HDNICGNSSTQKCGIDVTLCBEAFPRFAVPTKFTPMNLVAVDNLPGTKVNAESVERI 240
 Db 181 HDNICGNSSTQKCGIDVTLCBEAFPRFAVPTKFTPMNLVAVDNLPGTKVNAESVERI 240
 QY 241 KRQHSQEQTFQLLKLMKQNKDQIVKKIIDDIDLCENSVOHRIHGANLTFEQLSLME 300
 Db 241 KRQHSQEQTFQLLKLMKQNKDQIVKKIIDDIDLCENSVOHRIHGANLTFEQLSLME 300
 QY 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 Db 301 SLPGKVGADIEDIKTIKACPSDQILKLSLWRIKNGDDDTLKGMLHKGSTYHFPKT 360
 QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
 Db 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 12
US-10-377-076-1
Sequence 1, Application US/10377076
Publication No. US20030216297A1
GENERAL INFORMATION:
APPLICANT: Kumakura, Seichiro
APPLICANT: Nakajima, Tomoko
TITLE OF INVENTION: A Pharmaceutical Composition
FILE REFERENCE: 03117/HG
CURRENT APPLICATION NUMBER: US/10/377,076
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: JP 2002-055356
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNL
LOCATION: (-21)..(-1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (+1)..(+380)
OTHER INFORMATION:
US-10-377-076-1

Query Match 99.8%; Score 2195; DB 15; Length 401;
Best Local Similarity 99.8%; Pred. No. 2.2e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLICLVLDISIKTTQETPPPKYLHYDEETSHQLCDKCPGTYLKQHTAKMKT 60
DB 1 MNKLICLVLDISIKTTQETPPPKYLHYDEETSHQLCDKCPGTYLKQHTAKMKT 60
QY 61 VCAPCPDHYTDSWHTSECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCIK 120
DB 61 VCAPCPDHYTDSWHTSECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCIK 120
QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCEBAFFRPAVPTKFTPMWLSVLDNLPQTKVNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCEBAFFRPAVPTKFTPMWLSVLDNLPQTKVNAESVERI 240
QY 241 KROHSSOQOTQOLKLMWQNKDDIVKIIQDIDLCSNSVQRHIGHANLTFEQLRSIME 300
DB 241 KROHSSOQOTQOLKLMWQNKDDIVKIIQDIDLCSNSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPGKVAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKSKTYHFPKT 360
DB 301 SLPGKVAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKSKTYHFPKT 360
QY 361 VTQSLKTIKTIKIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401
DB 361 VTQSLKTIKTIKIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 13
US-10-785-109-5
Sequence 5, Application US/10785109
Publication No. US20040142426A1
GENERAL INFORMATION:
APPLICANT: GOTO, Masaaki
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, Nobuyuki
APPLICANT: SHIMA, Nobuyuki

APPLICANT: YASUDA, Hisataka
APPLICANT: NAKAGAWA, Nobuaki
APPLICANT: MORINAGA, Tomonori
APPLICANT: UEDA, Masatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
FILE REFERENCE: 16991.017
CURRENT APPLICATION NUMBER: US/10/785,109
CURRENT FILING DATE: 2004-02-25
PRIOR APPLICATION NUMBER: US 10/232,858
PRIOR FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 08/915,004
PRIOR FILING DATE: 1997-08-20
PRIOR APPLICATION NUMBER: PCT/JP96/00374
PRIOR FILING DATE: 1996-02-20
PRIOR APPLICATION NUMBER: JP 207508/1995
PRIOR FILING DATE: 1995-07-21
PRIOR APPLICATION NUMBER: JP 054977/1995
PRIOR FILING DATE: 1995-02-20
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-10-785-109-5

Query Match 99.8%; Score 2195; DB 16; Length 401;
Best Local Similarity 99.8%; Pred. No. 2.2e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNKLICLVLDISIKTTQETPPPKYLHYDEETSHQLCDKCPGTYLKQHTAKMKT 60
DB 1 MNKLICLVLDISIKTTQETPPPKYLHYDEETSHQLCDKCPGTYLKQHTAKMKT 60
QY 61 VCAPCPDHYTDSWHTSECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCIK 120
DB 61 VCAPCPDHYTDSWHTSECLYCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCIK 120
QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
QY 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPGGVVQAGTPEBNTVCKRCPDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNGSESTQKCGIDVTLCEBAFFRPAVPTKFTPMWLSVLDNLPQTKVNAESVERI 240
DB 181 HDNICSNGSESTQKCGIDVTLCEBAFFRPAVPTKFTPMWLSVLDNLPQTKVNAESVERI 240
QY 241 KROHSSOQOTQOLKLMWQNKDDIVKIIQDIDLCSNSVQRHIGHANLTFEQLRSIME 300
DB 241 KROHSSOQOTQOLKLMWQNKDDIVKIIQDIDLCSNSVQRHIGHANLTFEQLRSIME 300
QY 301 SLPGKVAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKSKTYHFPKT 360
DB 301 SLPGKVAEDIEKTIKACKPSDQILKLSLWRIKNGQDQTLKGLMHALKSKTYHFPKT 360
QY 361 VTQSLKTIKTIKIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401
DB 361 VTQSLKTIKTIKIRFLHSFTMYKLYQKLFLEMIGNOVOSVKISCL 401

RESULT 14
US-10-785-114-5
Sequence 5, Application US/10785114
Publication No. US20040143859A1
GENERAL INFORMATION:
APPLICANT: GOTO, Masaaki
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, Nobuyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: NAKAGAWA, Nobuaki

```

; APPLICANT: MORINAGA, Tomomori
; APPLICANT: UEDA, Masataugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OR INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.016
; CURRENT APPLICATION NUMBER: US/10/785,114
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-785-114-5

Query Match          99.8%; Score 2195; DB 16; Length 401;
Best Local Similarity 99.8%; Pred. No. 2,2e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEBESHQLLCDKCPGTYLKQHCIAKWK 60
DB 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEBESHQLLCDKCPGTYLKQHCIAKWK 60
QY 61 VCAPCPDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYIEIEFCLK 120
DB 61 VCAPCPDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYIEIEFCLK 120
QY 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
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DB 181 HDNICSNSSESTQKCGIDVTLCCEAFRRFAVPTKFTPNMLSVLVDNLPGTKVNAESVERI 240
QY 241 KRQSSQEQTFQLLKMKHQNKDQDIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
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QY 301 SLPGKTVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKPT 360
DB 301 SLPGKTVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKPT 360
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RESULT 15
US-09-405-032-125
; Sequence 125, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1640 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-405-032-125

Query Match          99.6%; Score 2192; DB 11; Length 401;
Best Local Similarity 99.8%; Pred. No. 3.9e-177;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEBESHQLLCDKCPGTYLKQHCIAKWK 60
DB 1 MNKLCCALVFLDISIKMTTQETFPKRYLHYDEBESHQLLCDKCPGTYLKQHCIAKWK 60
QY 61 VCAPCPDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYIEIEFCLK 120
DB 61 VCAPCPDHYTTDSWHTSDCLYCSPVCKELQYVQKQECNRTNHNVCCKEGRYIEIEFCLK 120
QY 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
DB 121 HRSCEPFGVQAGTBERNTVCRCPCDGFPSNETSKAPCRKHTNCSVFGILLTQKGNAT 180
QY 181 HDNICSNSSESTQKCGIDVTLCCEAFRRFAVPTKFTPNMLSVLVDNLPGTKVNAESVERI 240
DB 181 HDNICSNSSESTQKCGIDVTLCCEAFRRFAVPTKFTPNMLSVLVDNLPGTKVNAESVERI 240
QY 241 KRQSSQEQTFQLLKMKHQNKDQDIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
DB 241 KRQSSQEQTFQLLKMKHQNKDQDIVKIIQDIDLCENSVQRIHGHANLTFEQLRSIME 300
QY 301 SLPGKTVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKPT 360
DB 301 SLPGKTVGAEDEIKTIKACKPSDQILKLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKPT 360
QY 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401
DB 361 VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

Search completed: September 29, 2004, 12:45:45
Job time: 135 secs

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